



Full wwPDB EM Validation Report ⓘ

Jun 25, 2026 – 08:13 AM EDT

PDB ID : 9P6Z / pdb_00009p6z
EMDB ID : EMD-71329
Title : In situ human P-Z state 80S ribosome
Authors : Zheng, W.; Xiong, Y.
Deposited on : 2025-06-20
Resolution : 2.97 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

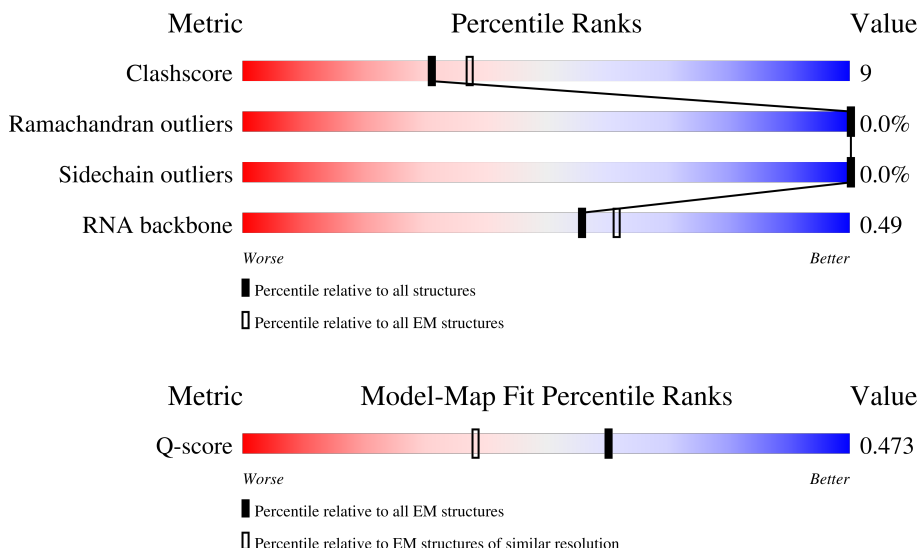
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.97 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13205 (2.47 - 3.47)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Pt	74	
2	L5	3655	
3	L7	120	

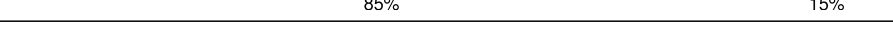
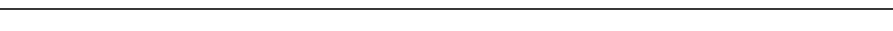
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Mol	Chain	Length	Quality of chain
4	L8	156	
5	LA	248	
6	LB	402	
7	LC	368	
8	LD	293	
9	LE	240	
10	LF	225	
11	LG	241	
12	LH	190	
13	LI	213	
14	LJ	176	
15	LL	210	
16	LM	139	
17	LN	203	
18	LO	201	
19	LP	153	
20	LQ	187	
21	LR	187	
22	LS	175	
23	LT	159	
24	LU	101	
25	LV	131	
26	LW	118	
27	LX	120	
28	LY	134	

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Mol	Chain	Length	Quality of chain
29	LZ	135	
30	La	147	
31	Lb	109	
32	Lc	98	
33	Ld	107	
34	Le	128	
35	Lf	109	
36	Lg	114	
37	Lh	122	
38	Li	102	
39	Lj	86	
40	Lk	69	
41	Ll	50	
42	Lm	52	
43	Ln	24	
44	Lo	105	
45	Lp	91	
46	Lr	125	
47	Ls	196	
48	Lt	141	
49	SD	227	
50	SF	189	
51	SK	98	
52	SM	122	
53	SP	121	

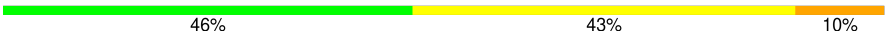
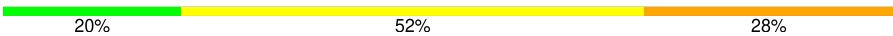
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Mol	Chain	Length	Quality of chain
54	SQ	144	
55	SR	135	
56	SS	145	
57	ST	143	
58	SU	104	
59	SZ	75	
60	Sc	64	
61	Sd	55	
62	Sf	67	
63	Sg	313	
64	SA	221	
65	SB	214	
66	SC	222	
67	SE	262	
68	SG	237	
69	SH	186	
70	SI	206	
71	SJ	185	
72	SL	153	
73	SN	150	
74	SO	140	
75	SV	83	
76	SW	129	
77	SX	141	
78	SY	131	

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Mol	Chain	Length	Quality of chain
79	Sa	102	 84% 16%
80	Sb	83	 66% 34%
81	Se	58	 5% 83% 17%
82	S2	1740	 46% 43% 10%
83	Zt	75	 20% 52% 28%
84	CI	31	 68% 32%

2 Entry composition [i](#)

There are 88 unique types of molecules in this entry. The entry contains 219971 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Pt	74	Total	C	N	O	P	0	0
			1576	705	286	512	73		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Pt	3	C	U	conflict	GB X64278
Pt	?	-	U	deletion	GB X64278
Pt	?	-	G	deletion	GB X64278
Pt	19	G	U	conflict	GB X64278
Pt	50	U	-	insertion	GB X64278
Pt	74	C	-	insertion	GB X64278

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L5	3655	Total	C	N	O	P	1	0
			78444	34968	14346	25475	3655		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 9 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LE	240	Total	C	N	O	S	0	0
			1935	1242	368	321	4		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	?	-	SER	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	VAL	deletion	UNP Q02878
LE	?	-	GLU	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878
LE	?	-	GLU	deletion	UNP Q02878
LE	?	-	LYS	deletion	UNP Q02878

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 11 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 13 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 15 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 17 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 18 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 20 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 22 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 24 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 26 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LW	116	Total	C	N	O	S	0	0
			945	592	193	156	4		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	?	-	SER	deletion	UNP A0A994J4A5
LW	?	-	GLU	deletion	UNP A0A994J4A5
LW	?	-	GLU	deletion	UNP A0A994J4A5
LW	?	-	ILE	deletion	UNP A0A994J4A5
LW	?	-	GLN	deletion	UNP A0A994J4A5
LW	?	-	LYS	deletion	UNP A0A994J4A5

- Molecule 27 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 28 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 30 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 31 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	PRO	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	GLU	deletion	UNP P47914
Lb	?	-	VAL	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	PRO	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	ILE	deletion	UNP P47914
Lb	?	-	PRO	deletion	UNP P47914
Lb	?	-	LYS	deletion	UNP P47914
Lb	?	-	GLY	deletion	UNP P47914

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 34 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 35 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 37 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 39 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 42 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 44 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 45 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 48 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lt	134	Total	C	N	O	S	0	0
			998	626	180	189	3		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lt	?	-	PRO	deletion	UNP P30050
Lt	?	-	PRO	deletion	UNP P30050
Lt	?	-	ARG	deletion	UNP P30050
Lt	?	-	ASP	deletion	UNP P30050
Lt	?	-	ARG	deletion	UNP P30050
Lt	?	-	LYS	deletion	UNP P30050
Lt	?	-	LYS	deletion	UNP P30050
Lt	?	-	GLN	deletion	UNP P30050
Lt	?	-	LYS	deletion	UNP P30050
Lt	?	-	ASN	deletion	UNP P30050
Lt	?	-	ILE	deletion	UNP P30050
Lt	?	-	LYS	deletion	UNP P30050
Lt	?	-	HIS	deletion	UNP P30050
Lt	?	-	SER	deletion	UNP P30050
Lt	?	-	GLY	deletion	UNP P30050
Lt	?	-	ASN	deletion	UNP P30050

- Molecule 49 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 50 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 51 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 52 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 54 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 55 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 56 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 57 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 58 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 59 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 60 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 61 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 62 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 63 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 64 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 65 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 66 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SC	220	Total	C	N	O	S	0	0
			1707	1104	293	300	10		

- Molecule 67 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 68 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 69 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SH	?	-	SER	deletion	UNP P62081
SH	?	-	ARG	deletion	UNP P62081
SH	?	-	THR	deletion	UNP P62081

- Molecule 70 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 71 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 72 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 73 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 74 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SO	137	Total	C	N	O	S	0	0
			1024	627	200	191	6		

- Molecule 75 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 76 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 77 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 80 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 81 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 82 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	S2	1740	Total	C	N	O	P	0	0
			36953	16508	6600	12106	1739		

- Molecule 83 is a RNA chain called Z site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Zt	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 84 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CI	31	Total	C	N	O	S	0	0
			247	153	55	38	1		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

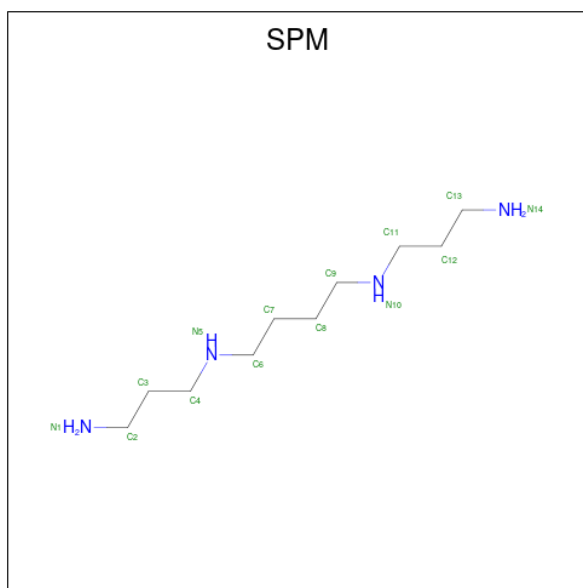
Mol	Chain	Residues	Atoms		AltConf
85	L5	179	Total	Mg	0
			179	179	
85	L7	3	Total	Mg	0
			3	3	
85	L8	5	Total	Mg	0
			5	5	

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Mol	Chain	Residues	Atoms		AltConf
85	LA	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	1	Total	Mg	0
			1	1	
85	SS	1	Total	Mg	0
			1	1	
85	SG	1	Total	Mg	0
			1	1	
85	S2	26	Total	Mg	0
			26	26	

- Molecule 86 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$) (labeled as "Ligand of Interest" by depositor).



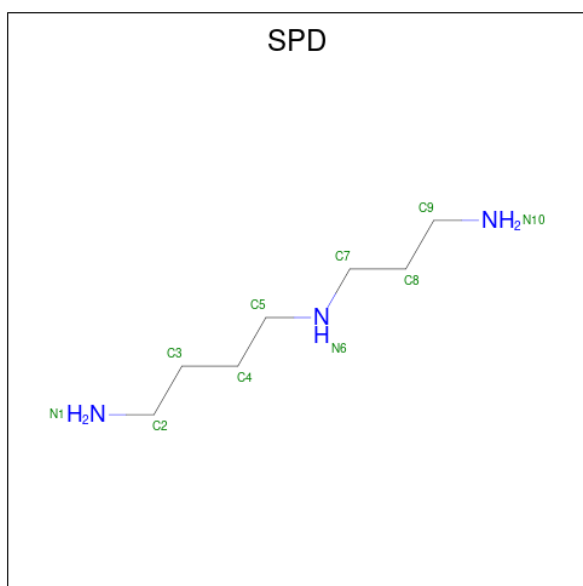
Mol	Chain	Residues	Atoms			AltConf
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	

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Mol	Chain	Residues	Atoms			AltConf
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	
86	L5	1	Total	C	N	0
			14	10	4	

- Molecule 87 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	

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Mol	Chain	Residues	Atoms			AltConf
87	L5	1	Total	C	N	0
			10	7	3	
87	L5	1	Total	C	N	0
			10	7	3	

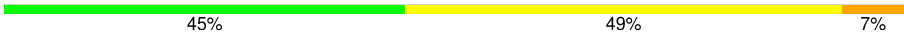
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total	Zn	0
			1	1	
88	Lj	1	Total	Zn	0
			1	1	
88	Lm	1	Total	Zn	0
			1	1	
88	Lo	1	Total	Zn	0
			1	1	
88	Lp	1	Total	Zn	0
			1	1	
88	Sa	1	Total	Zn	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

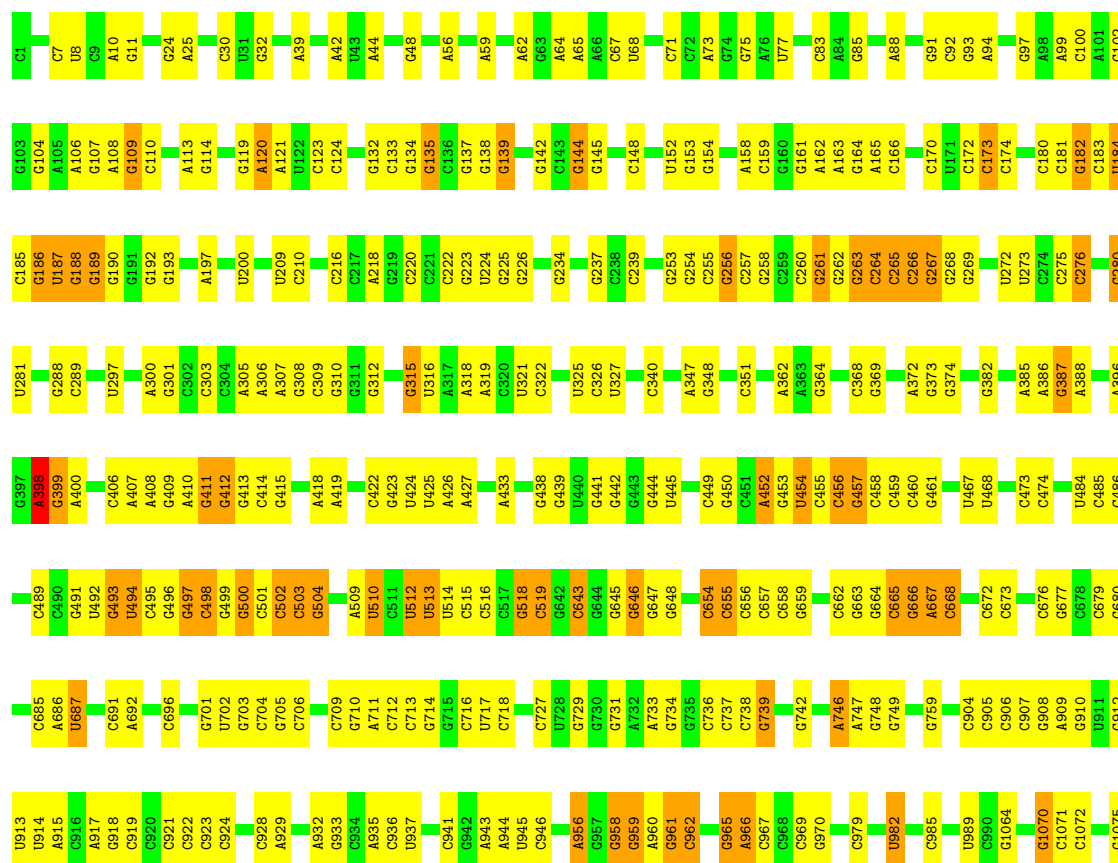
• Molecule 1: P site tRNA

Chain Pt: 



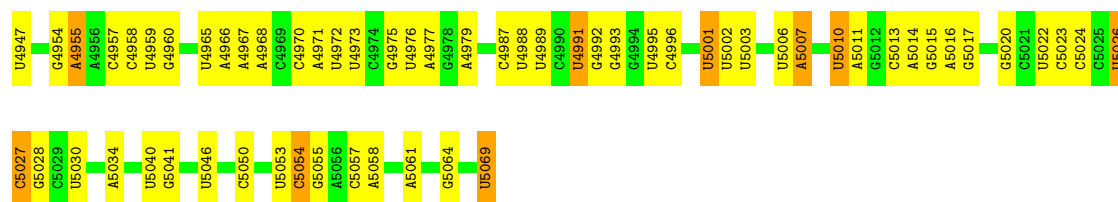
• Molecule 2: 28S rRNA

Chain L5: 



A2621	A2517	A2417	C2084	A1999	G1916	A1802	C1718	U1591	G1479	U1381	G1291	C1210	C1076
G2624	G2518	C2422	G2085	G2000	A1917	G1803	A1719	U1596	G1480	U1387	C1292	G1211	C1077
C2627	C2520	A2423	G2092	A2002	U1918	A1805	U1725	G1597	C1481	A1387	G1293	C1214	C1080
U2632	G2521	G2424	A2093	C2317	G1919	A1806	U1726	G1597	C1482	U1387	G1294	C1215	C1081
U2633	G2522	U2425	G2094	U2004	C1921	C1807	U1729	G1612	C1483	U1390	G1296	C1216	C1082
U2634	A2529	U2436	A2095	A2009	G1922	G1810	A1729	U1616	U1494	U1393	G1299	G1218	U1083
U2635	C2533	G2443	U2097	A2010	G1925	C1820	U1730	G1617	U1495	G1394	G1300	G1219	C1086
U2636	C2534	C2444	G2098	C2011	U1931	G1821	C1731	U1617	G1496	U1395	G1301	G1220	A1087
U2637	U2538	G2448	C2101	A2012	A1932	U1822	G1732	G1624	A1497	U1396	C1302	A1221	C1088
U2638	C2539	A2449	G2102	C2013	A1933	U1823	G1733	G1625	G1498	A1397	C1303	A1222	C1091
A2641	C2540	C2458	G2103	U2015	A1934	G1824	U1734	U1628	C1500	A1398	C1304	C1236	G1092
G2642	C2541	G2459	A2104	C2016	A1935	A1825	A1735	U1628	A1500	U1398	C1305	C1237	G1093
G2643	C2542	A2460	G2105	A2017	C1936	G1826	A1737	U1628	C1501	G1403	C1306	C1238	G1094
A2647	A2543	G2461	C2106	C2018	G1940	G1833	G1739	A1631	A1502	G1404	C1307	C1239	A1095
G2648	G2544	C2462	G2107	C2019	A1941	U1834	A1742	G1633	A1503	G1405	C1308	G1240	C1096
C2653	U2545	G2463	U2108	U2020	A1942	U1835	U1743	G1634	A1504	G1406	C1309	C1241	G1097
C2654	G2546	A2464	G2109	G2021	A1943	G1836	U1744	U1637	C1505	G1407	C1314	C1245	G1098
C2655	C2547	C2465	C2110	C2023	U1947	A1837	G1750	G1640	U1514	G1408	C1315	C1246	C1099
U2656	U2554	U2466	G2111	G2024	G1948	G1842	A1751	G1641	A1515	U1410	U1317	U1247	C1167
G2657	C2555	U2467	G2112	A2025	G1948	G1842	G1752	A1642	A1516	G1412	U1319	C1248	G1168
G2658	C2556	C2468	C2250	A2026	G1951	U1845	G1753	U1655	A1523	C1413	G1320	C1249	G1169
G2659	C2557	C2469	G2251	A2026	G1951	G1846	U1754	U1655	A1524	C1414	G1321	C1252	G1170
G2660	C2558	C2470	G2252	A2026	G1951	G1847	U1755	U1655	A1524	G1415	A1322	C1253	G1171
G2661	C2559	G2471	C2253	A2026	G1951	G1848	U1756	U1655	A1524	G1416	A1323	A1254	G1172
G2662	C2560	C2472	C2254	A2026	G1951	G1849	U1757	U1655	A1524	C1417	C1324	C1257	G1173
G2663	C2561	C2473	C2255	A2026	G1951	G1850	U1758	U1655	A1524	G1418	C1325	C1258	C1176
G2664	C2562	C2474	C2256	A2026	G1951	A1851	G1759	U1655	A1524	G1419	C1326	G1259	U1179
U2665	C2563	C2475	C2257	A2026	G1951	U1852	G1760	U1655	A1524	G1420	C1327	C1260	C1180
U2666	C2564	C2476	C2258	A2026	G1951	U1853	G1761	U1655	A1524	G1421	C1328	G1261	C1181
U2667	C2565	C2477	C2259	A2026	G1951	U1854	G1762	U1655	A1524	G1422	C1329	G1262	C1182
G2668	C2566	C2478	C2260	A2026	G1951	U1855	G1763	U1655	A1524	G1423	C1330	C1263	C1183
G2669	C2567	C2479	C2261	A2026	G1951	U1856	G1764	U1655	A1524	G1424	C1331	C1264	A1184
G2670	C2568	C2480	C2262	A2026	G1951	U1857	G1765	U1655	A1524	G1425	C1332	C1265	G1185
G2671	C2569	C2481	C2263	A2026	G1951	U1858	G1766	U1655	A1524	G1426	C1333	C1266	U1186
G2672	C2570	C2482	C2264	A2026	G1951	U1859	G1767	U1655	A1524	G1427	C1334	C1267	U1187
G2673	C2571	C2483	C2265	A2026	G1951	U1860	G1768	U1655	A1524	G1428	C1335	C1268	C1188
G2674	C2572	C2484	C2266	A2026	G1951	U1861	G1769	U1655	A1524	G1429	C1336	C1269	C1189
G2675	C2573	C2485	C2267	A2026	G1951	U1862	G1770	U1655	A1524	G1430	C1337	C1270	C1190
G2676	C2574	C2486	C2268	A2026	G1951	U1863	G1771	U1655	A1524	G1431	C1338	C1271	C1191
G2677	C2575	C2487	C2269	A2026	G1951	U1864	G1772	U1655	A1524	G1432	C1339	C1272	C1192
G2678	C2576	C2488	C2270	A2026	G1951	U1865	G1773	U1655	A1524	G1433	C1340	C1273	C1193
G2679	C2577	C2489	C2271	A2026	G1951	U1866	G1774	U1655	A1524	G1434	C1341	C1274	G1194
G2680	C2578	C2490	C2272	A2026	G1951	U1867	G1775	U1655	A1524	G1435	C1342	C1275	G1195
G2681	C2579	C2491	C2273	A2026	G1951	U1868	G1776	U1655	A1524	G1436	C1343	C1276	G1196
G2682	C2580	C2492	C2274	A2026	G1951	U1869	G1777	U1655	A1524	G1437	C1344	C1277	G1197
G2683	C2581	C2493	C2275	A2026	G1951	U1870	G1778	U1655	A1524	G1438	C1345	C1278	G1198
G2684	C2582	C2494	C2276	A2026	G1951	U1871	G1779	U1655	A1524	G1439	C1346	C1279	G1199
G2685	C2583	C2495	C2277	A2026	G1951	U1872	G1780	U1655	A1524	G1440	C1347	C1280	G1200
G2686	C2584	C2496	C2278	A2026	G1951	U1873	G1781	U1655	A1524	G1441	C1348	C1281	G1201
G2687	C2585	C2497	C2279	A2026	G1951	U1874	G1782	U1655	A1524	G1442	C1349	C1282	G1202
G2688	C2586	C2498	C2280	A2026	G1951	U1875	G1783	U1655	A1524	G1443	C1350	C1283	C1203
G2689	C2587	C2499	C2281	A2026	G1951	U1876	G1784	U1655	A1524	G1444	C1351	C1284	G1204
G2690	C2588	C2500	C2282	A2026	G1951	U1877	G1785	U1655	A1524	G1445	C1352	C1285	G1205
G2691	C2589	C2501	C2283	A2026	G1951	U1878	G1786	U1655	A1524	G1446	C1353	C1286	G1206
G2692	C2590	C2502	C2284	A2026	G1951	U1879	G1787	U1655	A1524	G1447	C1354	C1287	G1207
G2693	C2591	C2503	C2285	A2026	G1951	U1880	G1788	U1655	A1524	G1448	C1355	C1288	G1208
G2694	C2592	C2504	C2286	A2026	G1951	U1881	G1789	U1655	A1524	G1449	C1356	C1289	G1209
G2695	C2593	C2505	C2287	A2026	G1951	U1882	G1790	U1655	A1524	G1450	C1357	C1290	G1210
G2696	C2594	C2506	C2288	A2026	G1951	U1883	G1791	U1655	A1524	G1451	C1358	C1291	G1211
G2697	C2595	C2507	C2289	A2026	G1951	U1884	G1792	U1655	A1524	G1452	C1359	C1292	G1212
G2698	C2596	C2508	C2290	A2026	G1951	U1885	G1793	U1655	A1524	G1453	C1360	C1293	G1213
G2699	C2597	C2509	C2291	A2026	G1951	U1886	G1794	U1655	A1524	G1454	C1361	C1294	G1214
G2700	C2598	C2510	C2292	A2026	G1951	U1887	G1795	U1655	A1524	G1455	C1362	C1295	G1215
G2701	C2599	C2511	C2293	A2026	G1951	U1888	G1796	U1655	A1524	G1456	C1363	C1296	G1216
G2702	C2600	C2512	C2294	A2026	G1951	U1889	G1797	U1655	A1524	G1457	C1364	C1297	G1217
G2703	C2601	C2513	C2295	A2026	G1951	U1890	G1798	U1655	A1524	G1458	C1365	C1298	G1218
G2704	C2602	C2514	C2296	A2026	G1951	U1891	G1799	U1655	A1524	G1459	C1366	C1299	G1219
G2705	C2603	C2515	C2297	A2026	G1951	U1892	G1800	U1655	A1524	G1460	C1367	C1300	G1220
G2706	C2604	C2516	C2298	A2026	G1951	U1893	G1801	U1655	A1524	G1461	C1368	C1301	G1221
G2707	C2605	C2517	C2299	A2026	G1951	U1894	G1802	U1655	A1524	G1462	C1369	C1302	G1222
G2708	C2606	C2518	C2300	A2026	G1951	U1895	G1803	U1655	A1524	G1463	C1370	C1303	G1223
G2709	C2607	C2519	C2301	A2026	G1951	U1896	G1804	U1655	A1524	G1464	C1371	C1304	G1224
G2710	C2608	C2520	C2302	A2026	G1951	U1897	G1805	U1655	A1524	G1465	C1372	C1305	G1225
G2711	C2609	C2521	C2303	A2026	G1951	U1898	G1806	U1655	A1524	G1466	C1373	C1306	G1226
G2712	C2610	C2522	C2304	A2026	G1951	U1899	G1807	U1655	A1524	G1467	C1374	C1307	G1227
G2713	C2611	C2523	C2305	A2026	G1951	U1900	G1808	U1655	A1524	G1468	C1375	C1308	G1228
G2714	C2612	C2524	C2306	A2026	G1951	U1901	G1809	U1655	A1524	G1469	C1376	C1309	G1229
G2715	C2613	C2525	C2307	A2026	G1951	U1902	G1810	U1655	A1524	G1470	C1377	C1310	G1230
G2716	C2614	C2526	C2308	A2026	G1951	U1903	G1811	U1655	A1524	G1471	C1378	C1311	G1231
G2717	C2615	C2527	C2309	A2026	G1951	U1904	G1812	U1655	A1524	G1472	C1379	C1312	G1232
G2718	C2616	C2528	C2310	A2026	G1951	U1905	G1813	U1655	A1524	G1473	C1380	C1313	G1233
G2719	C2617	C2529	C2311	A2026	G1951	U1906	G1814	U1655	A1524	G1474	C1381	C1314	G1234
G2720	C2618	C2530	C2312	A2026	G1951	U1907	G1815	U1655	A1524	G1475	C1382	C1315	G1235
G2721	C2619	C2531	C2313	A2026	G1951	U1908	G1816	U1655	A1524	G1476	C1383	C1316	G1236
G2722	C2620	C2532	C2314	A2026	G1951	U1909	G1817	U1655	A1524	G1477	C1384	C1317	G1237
G2723	C2621	C2533	C2315	A2026	G1951	U1910	G1818	U1655	A1524	G1478	C1385	C1318	G1238
G2724	C2622	C2534	C2316	A2026	G1951	U1911	G1819	U1655	A1524	G1479	C1386	C1319	G1239
G2725	C2623	C2535	C2317	A2026	G1951	U1912	G1820	U1655	A1524	G1480	C1387	C1320	G1240
G2726	C2624	C2536	C2318	A2026	G1951	U1913	G1821	U1655	A1524	G1481	C1388	C1321	G1241
G2727	C2625	C2537	C2319	A2026	G1951	U1914	G1822	U1655	A1524	G1482	C1389	C1322	G1242
G2728	C2626	C2538	C2320	A2026	G1951	U1915	G1823	U1655	A1524	G1483	C1390	C1323	G1243
G2729	C2627	C2539	C2321	A2026	G1951	U1916	G1824	U1655	A1524	G1484	C1391	C1324	G1244
G2730	C2628	C2540	C2322	A2026	G1951	U1917	G1825	U16					

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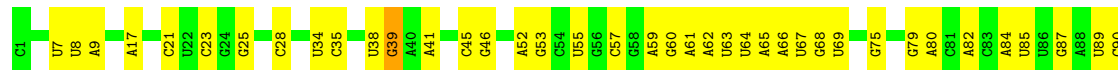
• Molecule 3: 5S rRNA

Chain L7: 74% 23%



• Molecule 4: 5.8S rRNA

Chain L8: 61% 36%



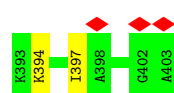
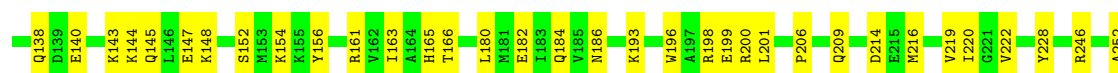
• Molecule 5: 60S ribosomal protein L8

Chain LA: 79% 21%

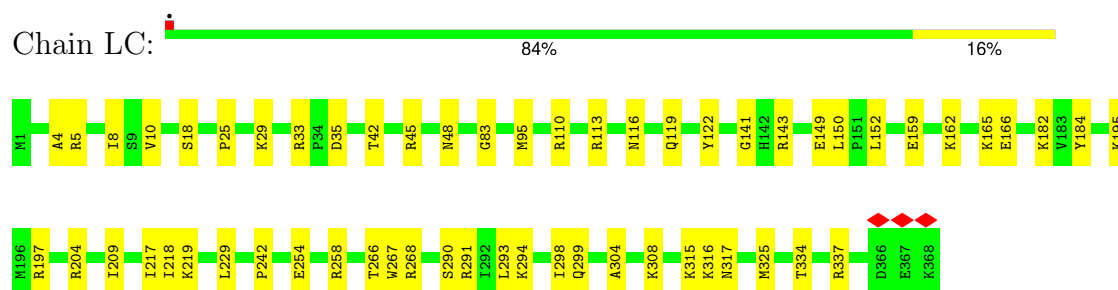


• Molecule 6: Large ribosomal subunit protein uL3

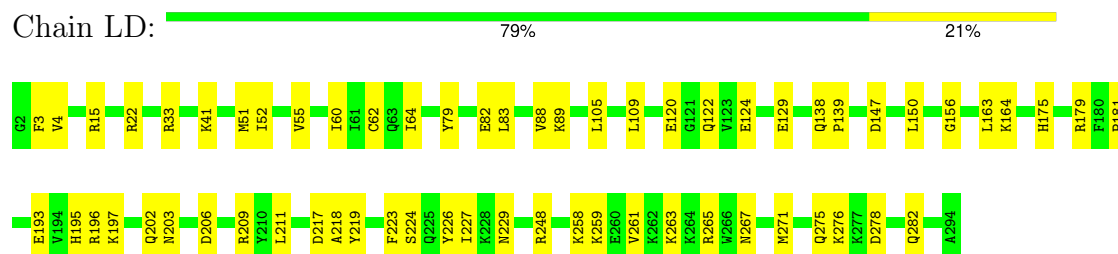
Chain LB: 74% 26%



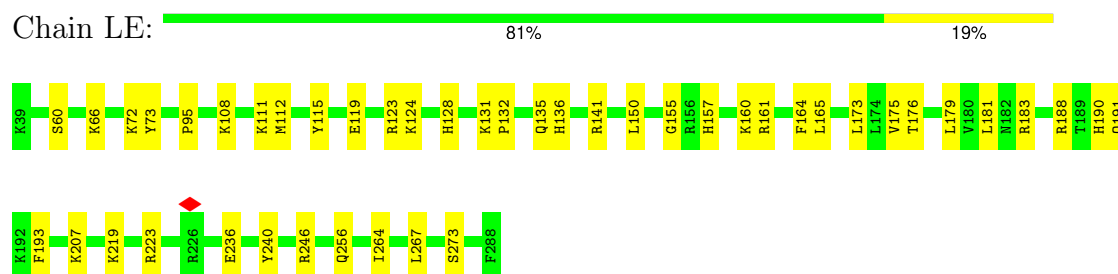
- Molecule 7: 60S ribosomal protein L4



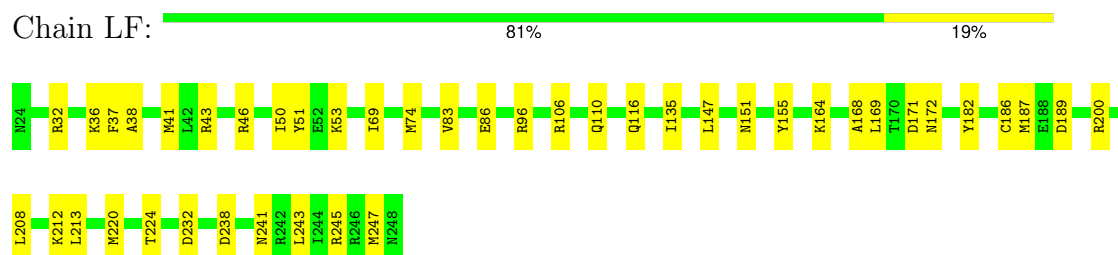
- Molecule 8: Large ribosomal subunit protein uL18



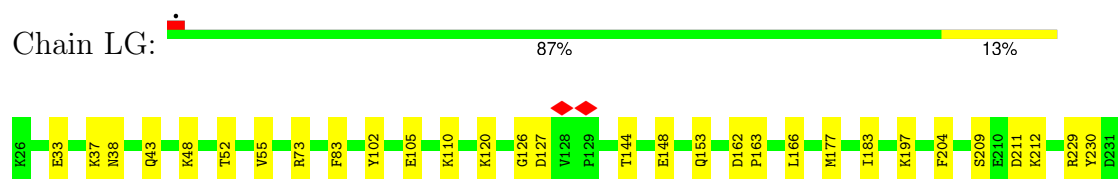
- Molecule 9: Large ribosomal subunit protein eL6

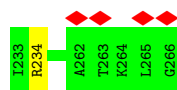


- Molecule 10: 60S ribosomal protein L7



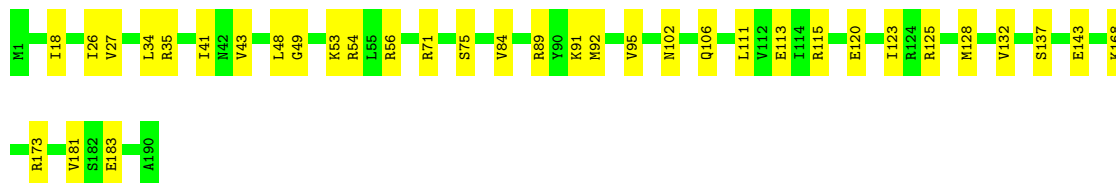
- Molecule 11: 60S ribosomal protein L7a





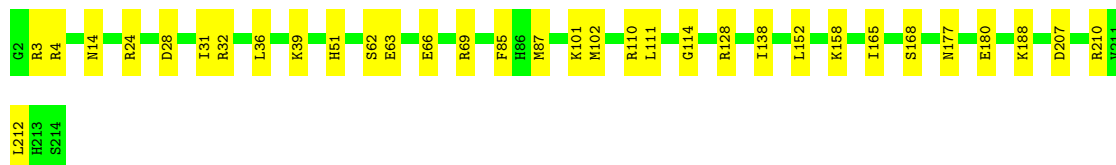
- Molecule 12: 60S ribosomal protein L9

Chain LH: 82% 18%



- Molecule 13: Ribosomal protein uL16-like

Chain LI: 85% 15%



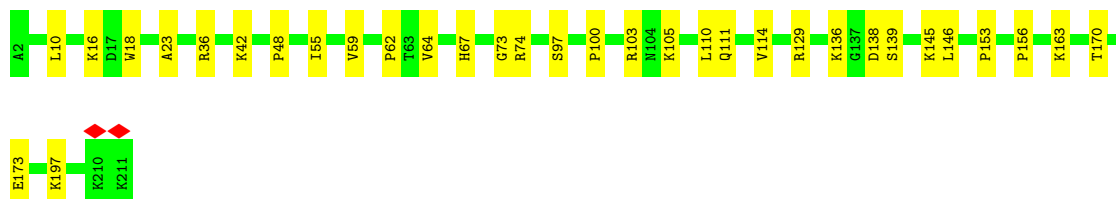
- Molecule 14: 60S ribosomal protein L11

Chain LJ: 70% 26%



- Molecule 15: Large ribosomal subunit protein eL13

Chain LL: 84% 16%



- Molecule 16: 60S ribosomal protein L14

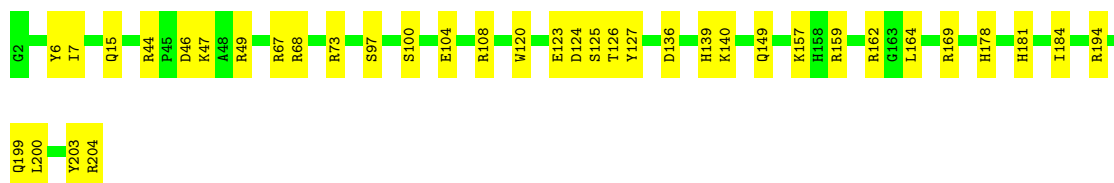
Chain LM: 80% 20%





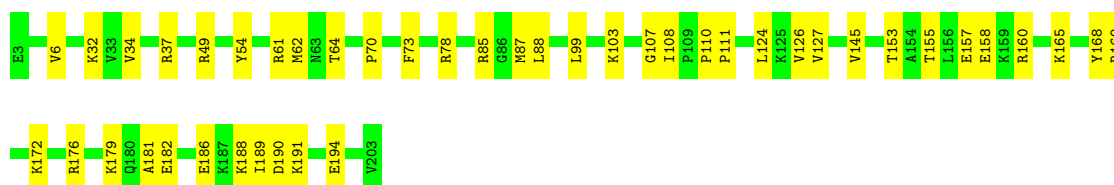
- Molecule 17: 60S ribosomal protein L15

Chain LN: 82% 18%



- Molecule 18: 60S ribosomal protein L13a

Chain LO: 78% 22%



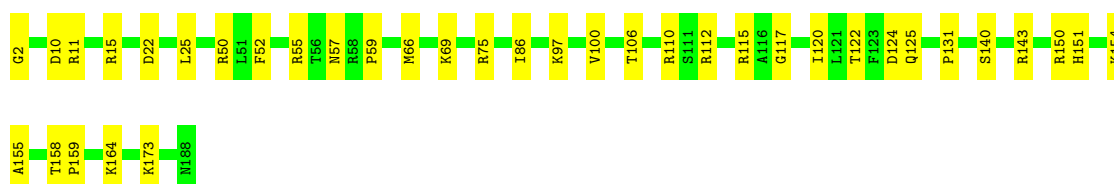
- Molecule 19: 60S ribosomal protein L17

Chain LP: 84% 16%



- Molecule 20: 60S ribosomal protein L18

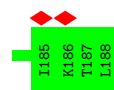
Chain LQ: 80% 20%



- Molecule 21: 60S ribosomal protein L19

Chain LR: 83% 17%





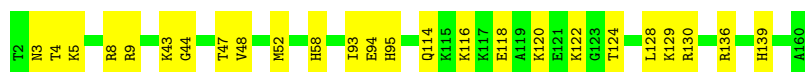
- Molecule 22: 60S ribosomal protein L18a

Chain LS: 87% 13%



- Molecule 23: 60S ribosomal protein L21

Chain LT: 84% 16%



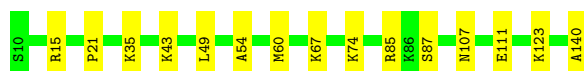
- Molecule 24: Heparin-binding protein HBp15

Chain LU: 70% 30%



- Molecule 25: 60S ribosomal protein L23

Chain LV: 89% 11%



- Molecule 26: Ribosomal protein L24

Chain LW: 75% 24%



- Molecule 27: 60S ribosomal protein L23a

Chain LX: 79% 21%

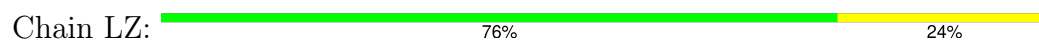


- Molecule 28: 60S ribosomal protein L26

Chain LY: 84% 16%



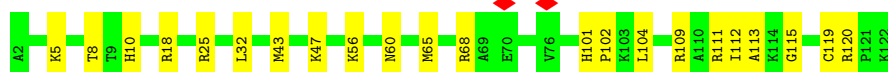
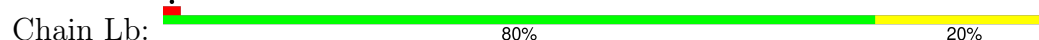
- Molecule 29: 60S ribosomal protein L27



- Molecule 30: 60S ribosomal protein L27a



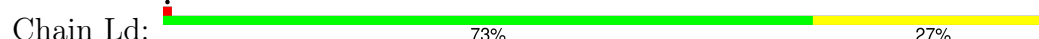
- Molecule 31: Large ribosomal subunit protein eL29



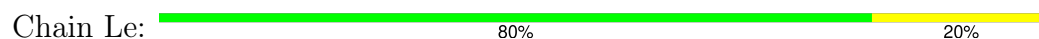
- Molecule 32: 60S ribosomal protein L30



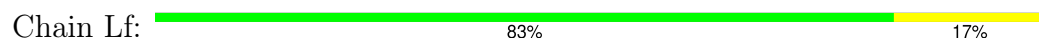
- Molecule 33: 60S ribosomal protein L31



- Molecule 34: 60S ribosomal protein L32

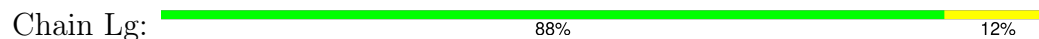


- Molecule 35: 60S ribosomal protein L35a

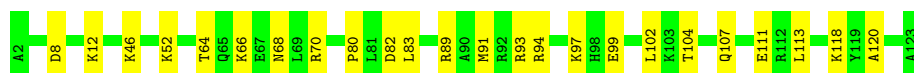
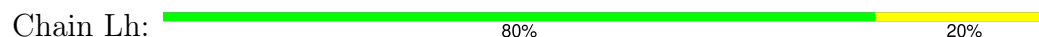




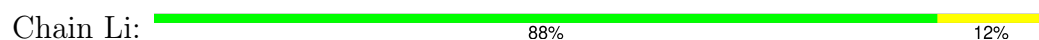
- Molecule 36: 60S ribosomal protein L34



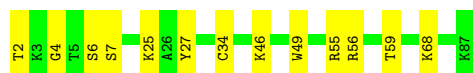
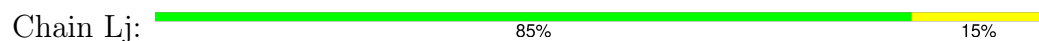
- Molecule 37: 60S ribosomal protein L35



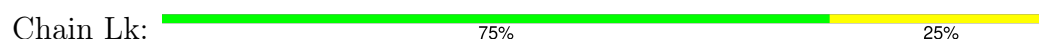
- Molecule 38: 60S ribosomal protein L36



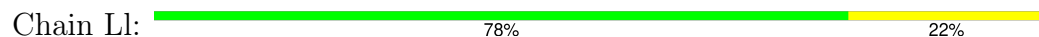
- Molecule 39: 60S ribosomal protein L37



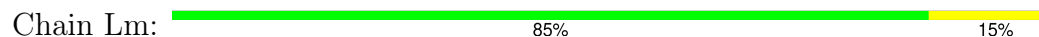
- Molecule 40: 60S ribosomal protein L38



- Molecule 41: 60S ribosomal protein L39



- Molecule 42: Large ribosomal subunit protein eL40





- Molecule 43: 60S ribosomal protein L41

Chain Ln: 79% 21%



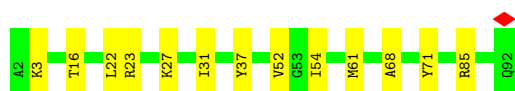
- Molecule 44: 60S ribosomal protein L36a

Chain Lo: 80% 20%



- Molecule 45: 60S ribosomal protein L37a

Chain Lp: 86% 14%



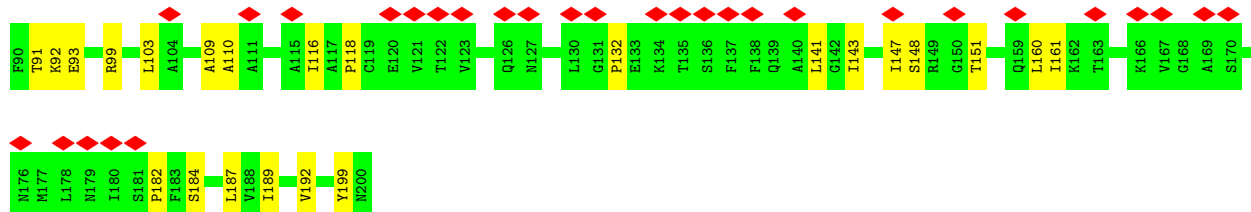
- Molecule 46: 60S ribosomal protein L28

Chain Lr: 81% 19%

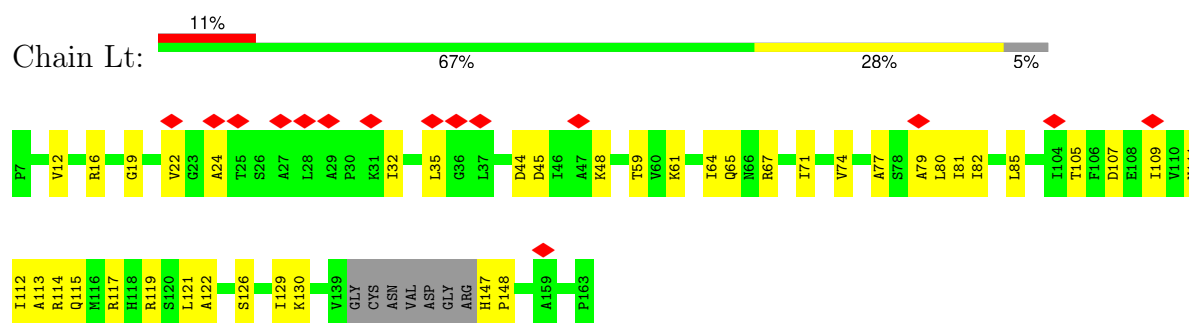


- Molecule 47: 60S acidic ribosomal protein P0

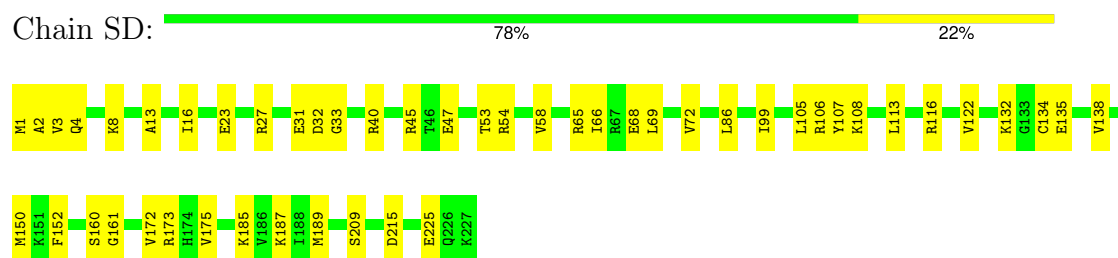
Chain Ls: 16% 69% 31%



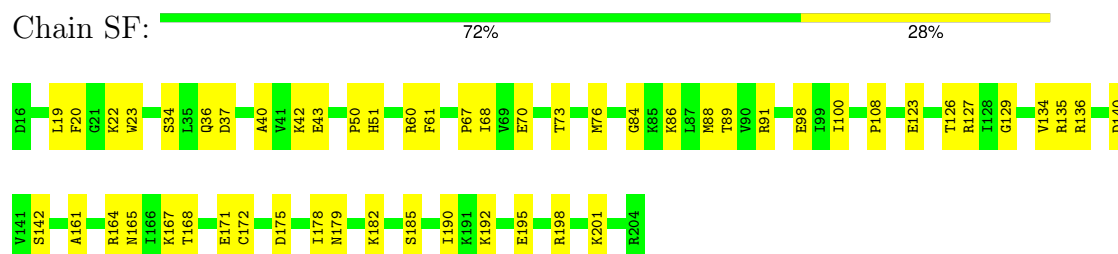
- Molecule 48: Large ribosomal subunit protein uL11



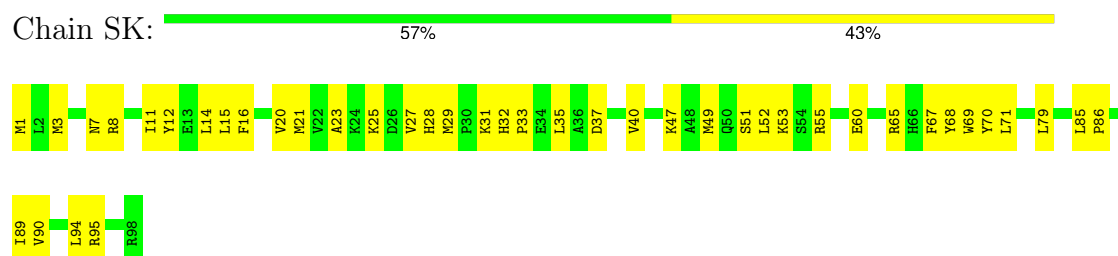
- Molecule 49: Small ribosomal subunit protein uS3



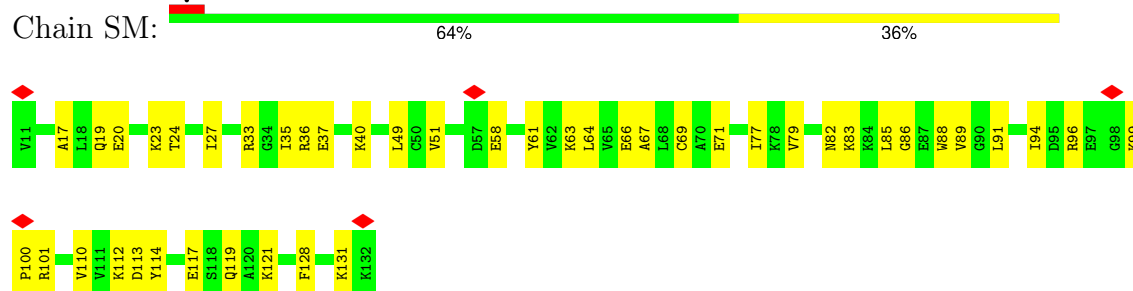
- Molecule 50: 40S ribosomal protein S5



- Molecule 51: 40S ribosomal protein S10

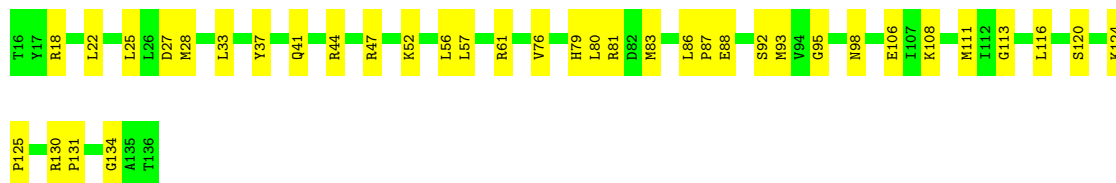


- Molecule 52: Small ribosomal subunit protein eS12



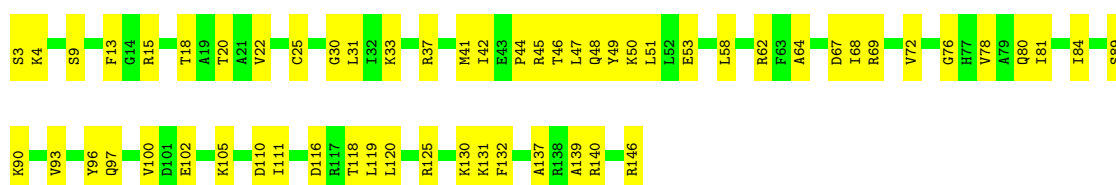
- Molecule 53: Small ribosomal subunit protein uS19

Chain SP:  69% 31%



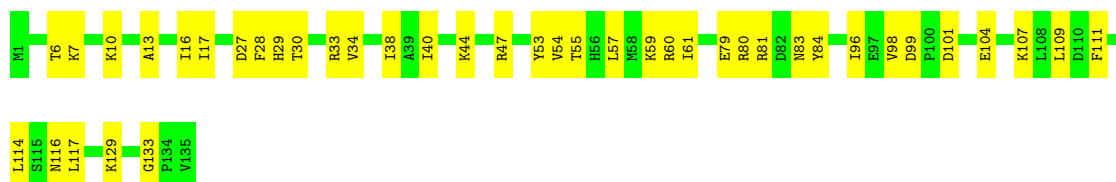
- Molecule 54: Small ribosomal subunit protein uS9

Chain SQ:  60% 40%



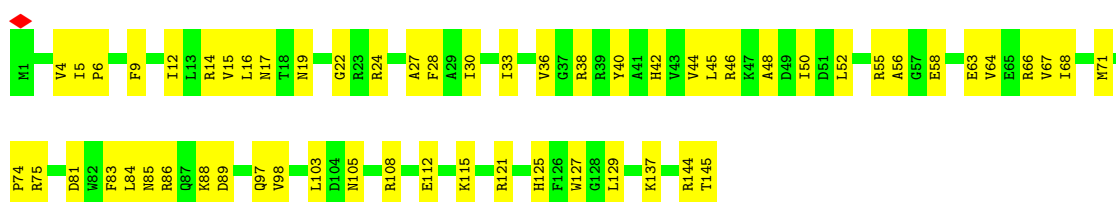
- Molecule 55: Small ribosomal subunit protein eS17

Chain SR:  70% 30%



- Molecule 56: 40S ribosomal protein S18

Chain SS:  60% 40%



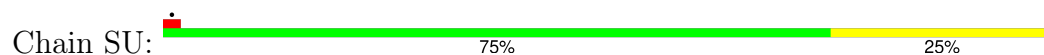
- Molecule 57: 40S ribosomal protein S19

Chain ST:  71% 29%





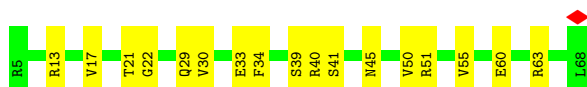
- Molecule 58: 40S ribosomal protein S20



- Molecule 59: Small ribosomal subunit protein eS25



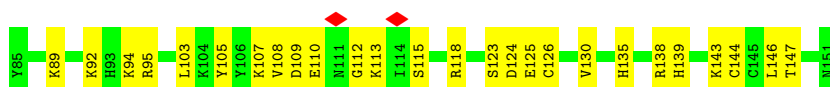
- Molecule 60: 40S ribosomal protein S28



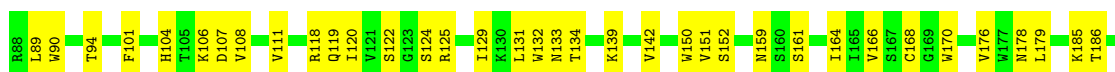
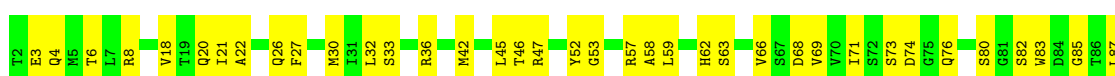
- Molecule 61: 40S ribosomal protein S29



- Molecule 62: Ubiquitin-40S ribosomal protein S27a

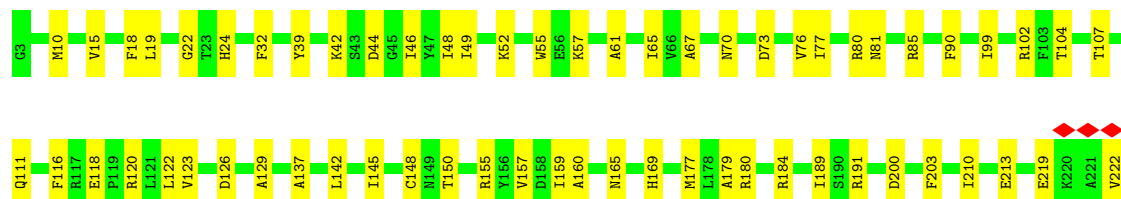


- Molecule 63: Receptor of activated protein C kinase 1

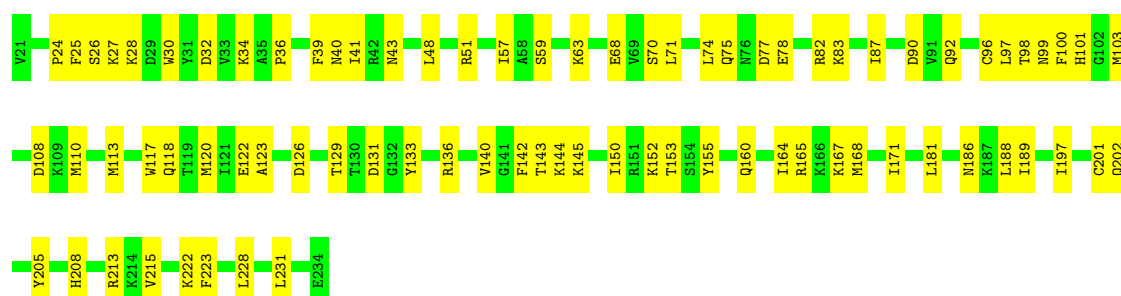




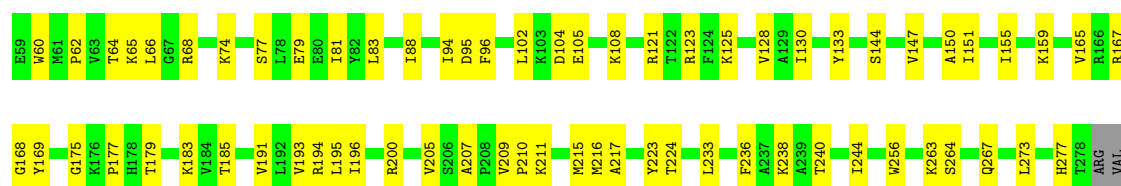
• Molecule 64: 40S ribosomal protein SA



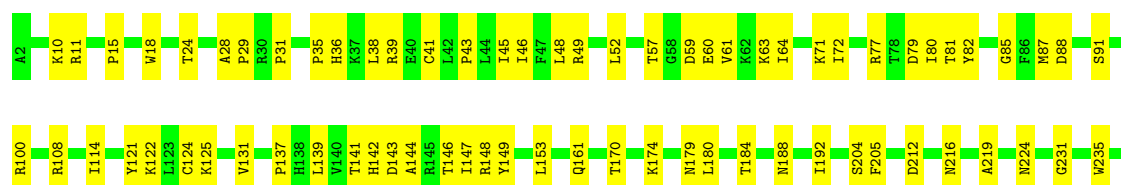
• Molecule 65: 40S ribosomal protein S3a

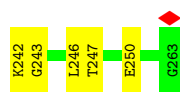


• Molecule 66: 40S ribosomal protein S2



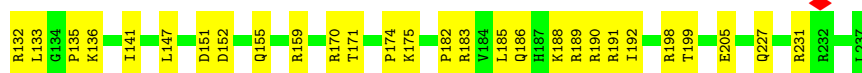
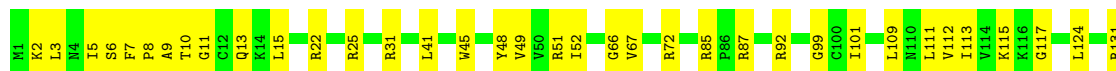
• Molecule 67: Small ribosomal subunit protein eS4, X isoform





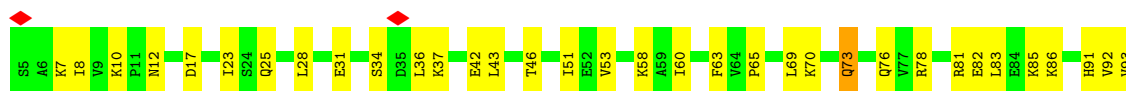
- Molecule 68: 40S ribosomal protein S6

Chain SG: 73% 27%



- Molecule 69: Small ribosomal subunit protein eS7

Chain SH: 66% 33%



- Molecule 70: 40S ribosomal protein S8

Chain SI: 71% 29%



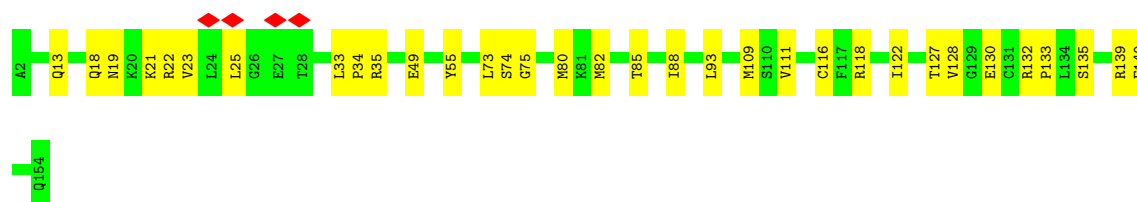
- Molecule 71: 40S ribosomal protein S9

Chain SJ: 82% 18%



- Molecule 72: 40S ribosomal protein S11

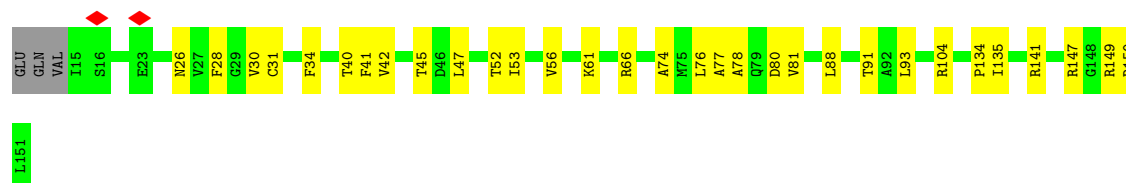
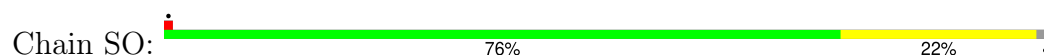
Chain SL: 78% 22%



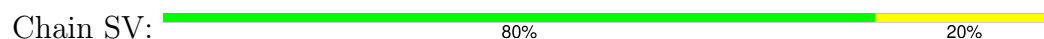
- Molecule 73: 40S ribosomal protein S13



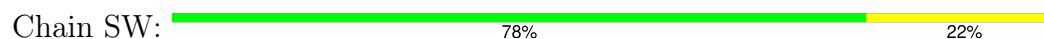
- Molecule 74: Small ribosomal subunit protein uS11



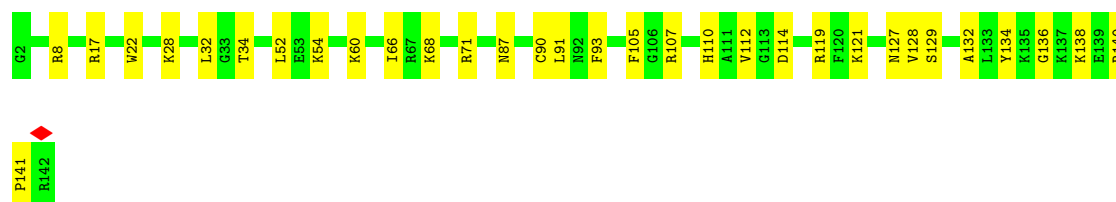
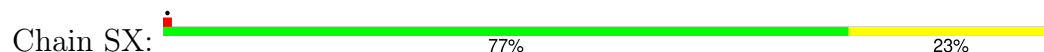
- Molecule 75: Small ribosomal subunit protein eS21



- Molecule 76: 40S ribosomal protein S15a

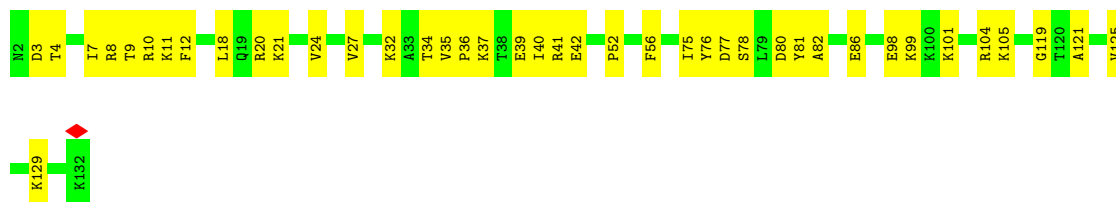


- Molecule 77: 40S ribosomal protein S23



- Molecule 78: 40S ribosomal protein S24

Chain SY:  69% 31%



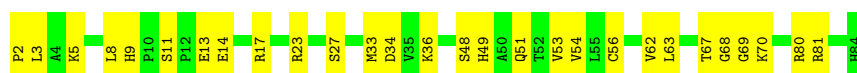
- Molecule 79: 40S ribosomal protein S26

Chain Sa:  84% 16%



- Molecule 80: Small ribosomal subunit protein eS27

Chain Sb:  66% 34%

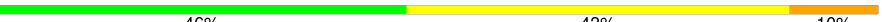


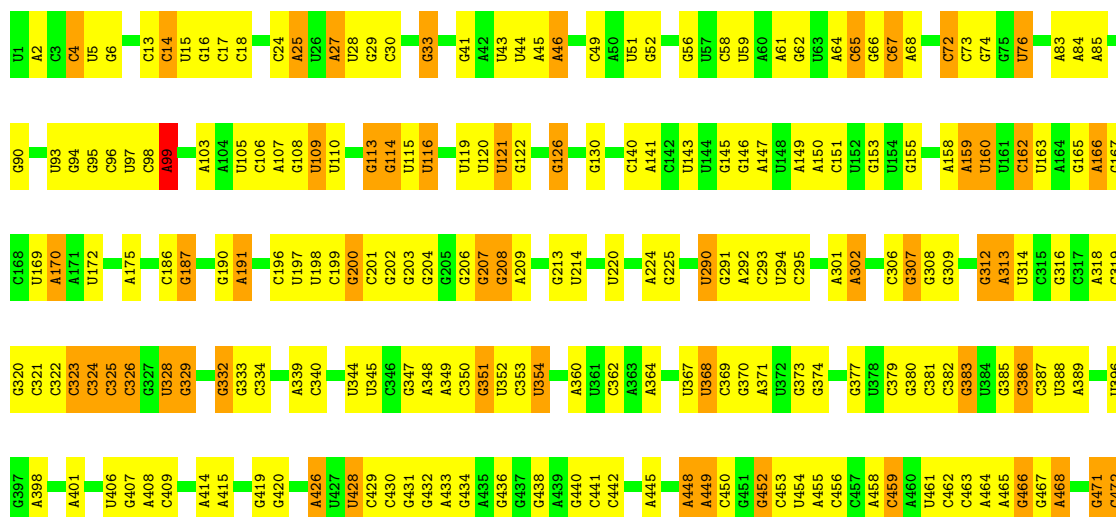
- Molecule 81: Small ribosomal subunit protein eS30

Chain Se:  5% 83% 17%

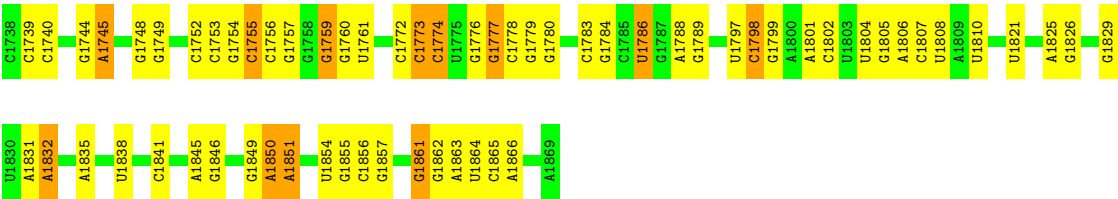


- Molecule 82: 18S rRNA

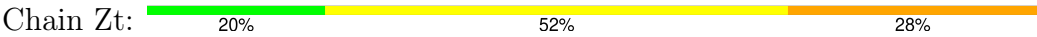
Chain S2:  46% 43% 10%



G1652	U1578	C1501	G1406	A1313	A1241	G1158	A1083	C989	G910	C842	C736	C639	A473
U1653	A1579	C1502	U1407	U1314	U1242	A1170	A1084	A990	A913	C843	G737	C640	G474
C1654	C1580	G1502	U1408	G1320	U1243	A1171	G1085	G991	A914	U844	C738	A641	C475
G1656	C1581	A1506	U1409	G1321	U1244	U1173	G1086	G992	A915	U845	C739	U652	A476
G1657	C1582	G1507	C1410	G1322	B8U1248	U1174	U1087	G993	A916	U846	C740	U642	G482
G1658	G1584	G1508	G1411	U1323	G1248	G1175	U1088	A994	G917	U847	C741	A643	C483
C1659	U1585	C1512	G1413	U1324	A1251	G1176	G1089	A995	G918	A848	C742	U644	A484
U1660	U1586	C1513	C1416	G1325	C1252	U1177	G1090	A996	G919	C851	U749	U647	A485
A1661	G1587	C1417	C1418	G1326	A1253	U1178	C1091	A997	G920	C852	C750	G558	A486
U1662	A1588	C1418	G1327	U1327	C1254	G1179	G1092	C1000	G921	G853	C751	G559	U487
A1663	C1589	U1518	G1328	G1328	G1255	G1180	A1093	G922	G922	G854	C752	A560	A488
G1664	U1590	C1519	G1329	G1329	G1256	G1181	U1101	A1001	G923	G855	C753	U651	
C1665	G1520	U1520	G1420	U1330	G1257	A1182	G1096	U1002	G924	G856	C754	U652	C492
C1666	C1521	A1522	A1421	U1331	G1258	A1183	G1097	U1003	G925	U857	C755	U653	A493
U1667	C1522	G1338	C1422	G1338	A1259	A1184	C1098	U1004	G926	A858	C756	A564	A494
U1668	C1523	G1339	C1423	G1339	A1260	A1185	G1099	A1005	G927	C931	C757	U655	C494
G1669	G1524	U1340	C1424	U1340	A1261	A1186	U1101	A1006	G928	G859	C758	U656	U495
C1670	G1525	U1341	C1425	U1341	G1262	A1187	U1102	A1007	G929	G860	C759	G566	U496
G1671	U1526	U1342	C1426	U1342	A1263	A1188	G1102	A1008	G930	U861	C760	C570	C497
U1672	G1527	U1343	C1427	U1343	A1264	A1189	G1103	A1009	G931	U862	C761	U657	
G1673	U1528	U1344	C1428	U1344	A1265	A1190	G1104	A1010	G932	U863	C762	U658	A500
U1674	G1529	U1345	C1429	U1345	A1266	A1191	G1105	A1011	G933	U864	C763	U659	C502
C1675	U1530	U1346	C1430	U1346	A1267	A1192	G1106	A1012	G934	U865	C764	U660	G507
G1676	U1531	U1347	C1431	U1347	A1268	U1193	G1107	A1013	G935	U866	C765	U661	A508
U1677	U1532	U1348	C1432	U1348	A1269	A1194	G1108	U1014	G936	U867	C766	U662	G509
G1678	U1533	U1349	C1433	U1349	A1270	A1195	G1109	U1015	G937	U868	C767	U663	C510
C1679	C1534	U1350	C1434	U1350	A1271	A1196	G1110	U1016	G938	U869	C768	U664	A512
G1680	U1535	U1351	C1435	U1351	A1272	A1197	G1111	U1017	G939	U870	C769	U665	G517
U1681	U1536	U1352	C1436	U1352	A1273	A1198	G1112	U1018	G940	U871	C770	U666	G518
C1682	C1537	U1353	C1437	U1353	A1274	A1199	G1113	U1019	G941	U872	C771	U667	A519
G1683	U1538	U1354	C1438	U1354	A1275	A1200	G1114	U1020	G942	U873	C772	U668	A520
C1684	A1539	U1355	C1439	U1355	A1276	U1201	G1115	U1021	G943	U874	C773	U669	A521
U1685	G1540	U1356	C1440	U1356	A1277	U1202	G1116	U1022	G944	U875	C774	U670	A522
G1686	U1541	U1357	C1441	U1357	A1278	U1203	G1117	U1023	G945	U876	C775	U671	C517
U1687	G1542	U1358	C1442	U1358	A1279	U1204	G1118	U1024	G946	U877	C776	U672	G518
C1688	C1543	U1359	C1443	U1359	A1280	U1205	G1119	U1025	G947	U878	C777	U673	A519
U1689	U1544	U1360	C1444	U1360	A1281	A1206	G1120	U1026	G948	U879	C778	U674	A520
A1690	G1545	U1361	C1445	U1361	A1282	A1207	G1121	A1027	G949	U880	C779	U675	A512
C1691	U1546	U1362	C1446	U1362	A1283	U1208	G1122	U1028	G950	U881	C780	U676	C517
U1692	G1547	U1363	C1447	U1363	A1284	A1209	G1123	U1029	G951	U882	C781	U677	G518
G1693	U1548	U1364	C1448	U1364	A1285	A1210	G1124	U1030	G952	U883	C782	U678	A519
C1694	U1549	U1365	C1449	U1365	A1286	A1211	G1125	U1031	G953	U884	C783	U679	A520
U1695	G1550	U1366	C1450	U1366	A1287	A1212	G1126	U1032	G954	U885	C784	U680	A521
G1696	U1551	U1367	C1451	U1367	A1288	A1213	G1127	U1033	G955	U886	C785	U681	A522
U1697	C1552	U1368	C1452	U1368	A1289	A1214	G1128	U1034	G956	U887	C786	U682	C517
C1698	U1553	U1369	C1453	U1369	A1290	A1215	G1129	U1035	G957	U888	C787	U683	G518
U1699	C1554	U1370	C1454	U1370	A1291	A1216	G1130	U1036	G958	U889	C788	U684	A519
G1700	U1555	U1371	C1455	U1371	A1292	A1217	G1131	U1037	G959	U890	C789	U685	A520
U1701	C1556	U1372	C1456	U1372	A1293	A1218	G1132	A1036	G960	U891	C790	U686	A521
C1702	U1557	U1373	C1457	U1373	A1294	A1219	G1133	U1037	G961	U892	C791	U687	A522
G1703	U1558	U1374	C1458	U1374	A1295	A1220	G1134	U1038	G962	U893	C792	U688	C517
C1704	C1559	U1375	C1459	U1375	A1296	A1221	G1135	U1039	G963	U894	C793	U689	G518
U1705	U1560	U1376	C1460	U1376	A1297	A1222	G1136	U1040	G964	U895	C794	U690	A519
G1706	C1561	U1377	C1461	U1377	A1298	A1223	G1137	U1041	G965	U896	C795	U691	A520
U1707	U1562	U1378	C1462	U1378	A1299	A1224	G1138	U1042	G966	U897	C796	U692	A521
C1708	C1563	U1379	C1463	U1379	A1300	A1225	G1139	U1043	G967	U898	C797	U693	A522
U1709	U1564	U1380	C1464	U1380	A1301	A1226	G1140	U1044	G968	U899	C798	U694	C517
G1710	C1565	U1381	C1465	U1381	A1302	A1227	G1141	U1045	G969	U900	C799	U695	U540
U1711	U1566	U1382	C1466	U1382	A1303	A1228	G1142	U1046	G970	C901	C800	U696	U541
C1712	C1567	U1383	C1467	U1383	A1304	A1229	G1143	U1047	G971	U901	C801	U697	U542
U1713	U1568	U1384	C1468	U1384	A1305	A1230	G1144	U1048	G972	U902	C802	U698	C543
G1714	C1569	U1385	C1469	U1385	A1306	A1231	G1145	U1049	G973	U903	C803	U699	C544
U1715	U1570	U1386	C1470	U1386	A1307	A1232	G1146	U1050	G974	U904	C804	U700	A536
C1716	C1571	U1387	C1471	U1387	A1308	A1233	G1147	U1051	G975	U905	C805	U701	C537
U1717	U1572	U1388	C1472	U1388	A1309	A1234	G1148	U1052	G976	U906	C806	U702	U540
G1718	C1573	U1389	C1473	U1389	A1310	A1235	G1149	U1053	G977	U907	C807	U703	U541
U1719	U1574	U1390	C1474	U1390	A1311	A1236	G1150	U1054	G978	U908	C808	U704	U542
C1720	C1575	U1391	C1475	U1391	A1312	A1237	G1151	U1055	G979	U909	C809	U705	C543
U1721	U1576	U1392	C1476	U1392	A1313	A1238	G1152	U1056	G980	U910	C810	U706	A536
G1722	C1577	U1393	C1477	U1393	A1314	A1239	G1153	U1057	G981	U911	C811	U707	C537
U1723	U1578	U1394	C1478	U1394	A1315	A1240	G1154	U1058	G982	U912	C812	U708	U540
C1724	C1579	U1395	C1479	U1395	A1316	A1241	G1155	U1059	G983	U913	C813	U709	U541
U1725	U1580	U1396	C1480	U1396	A1317	A1242	G1156	U1060	G984	U914	C814	U710	C543
G1726	C1581	U1397	C1481	U1397	A1318	A1243	G1157	U1061	G985	U915	C815	U711	A546
U1727	U1582	U1398	C1482	U1398	A1319	A1244	G1158	U1062	G986	U916	C816	U712	U546
C1728	C1583	U1399	C1483	U1399	A1320	A1245	G1159	U1063	G987	U917	C817	U713	G546
U1729	U1584	U1400	C1484	U1400	A1321	A1246	G1160	U1064	G988	U918	C818	U714	U547
G1730	C1585	U1401	C1485	U1401	A1322	A1247	G1161	U1065	G989	U919	C819	U715	C548
U1731	U1586	U1402	C1486	U1402	A1323	A1248	G1162	U1066	G990	U920	C820	U716	
G1732	C1587	U1403	C1487	U1403	A1324	A1249	G1163	U1067	G991	U921	C821	U717	
U1733	U1588	U1404	C1488	U1404	A1325	A1250	G1164	U1068	G992	U922	C822	U718	
C1734	C1589	U1405	C1489	U1405	A1326	A1251	G1165	U1069	G993	U923	C823	U719	
U1735	U1590	U1406	C1490	U1406	A1327	A1252	G1166	U1070	G994	U924	C824	U720	
G1736	C1591	U1407	C1491	U1407	A1328	A1253	G1167	U1071	G995	U925	C825	U721	
U1737	U1592	U1408	C1492	U1408	A1329	A1254	G1168	U1072	G996	U926	C826	U722	
G1738	C1593	U1409	C1493	U1409	A1330	A1255	G1169	U1073	G997	U927	C827	U723	
U1739	U1594	U1410	C1494	U1410	A1331	A1256	G1170	U1074	G998	U928	C828	U724	
C1740	C1595	U1411	C1495	U1411	A1332	A1257	G1171	U1075	G999	U929	C829	U725	
U1741	U1596	U1412	C1496	U1412	A1333	A1258	G1172	U1076	G1000	U930	C830	U726	
G1742	C1597	U1413	C1497	U1413	A1334	A1259	G1173	U1077	G1001	U931	C831	U727	
U1743	U1598	U1414	C1498	U1414	A1335	A1260	G1174	U1078	G1002	U932	C832	U728	
C1744	C1599	U1415	C1499	U1415	A1336	A1261	G1175	U1079	G1003	U933	C833	U729	
U1745	U1600	U1416	C1500	U1416	A1337	A1262	G1176	U1080	G1004	U934	C834	U730	
G1746	C1601	U1417	C1501	U1417	A1338	A1263	G1177	U1081	G1005	U935	C835	U731	
U1747	U1602	U1418	C1502	U1418	A1								



• Molecule 83: Z site tRNA



• Molecule 84: Transcription factor BTF3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23406	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.141	Depositor
Minimum map value	-0.065	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MA6, B8N, MG, 6MZ, PSU, A2M, 5MC, UY1, 4AC, OMG, SPM, OMC, 1MA, OMU, SPD, G7M, ZN, UR3

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Pt	0.19	0/1761	0.28	0/2741
2	L5	0.31	0/85098	0.32	0/132762
3	L7	0.29	0/2861	0.27	0/4459
4	L8	0.30	0/3631	0.29	0/5657
5	LA	0.32	0/1936	0.43	0/2596
6	LB	0.29	0/3306	0.39	0/4424
7	LC	0.29	0/2981	0.39	0/4002
8	LD	0.26	0/2428	0.38	0/3252
9	LE	0.25	0/1973	0.42	0/2645
10	LF	0.31	0/1905	0.40	0/2539
11	LG	0.25	0/1960	0.41	0/2637
12	LH	0.26	0/1537	0.39	0/2066
13	LI	0.25	0/1751	0.37	0/2340
14	LJ	0.25	0/1385	0.43	0/1852
15	LL	0.25	0/1732	0.37	0/2315
16	LM	0.29	0/1161	0.41	0/1554
17	LN	0.31	0/1746	0.35	0/2338
18	LO	0.31	0/1682	0.40	0/2250
19	LP	0.30	0/1268	0.43	0/1701
20	LQ	0.30	0/1537	0.38	0/2052
21	LR	0.25	0/1582	0.40	0/2091
22	LS	0.29	0/1493	0.36	0/2003
23	LT	0.30	0/1326	0.40	0/1770
24	LU	0.25	0/839	0.51	0/1126
25	LV	0.27	0/993	0.38	0/1332
26	LW	0.23	0/959	0.42	0/1270
27	LX	0.27	0/1002	0.39	0/1345
28	LY	0.28	0/1132	0.41	0/1504
29	LZ	0.26	0/1130	0.38	0/1507
30	La	0.29	0/1191	0.34	0/1591
31	Lb	0.23	0/889	0.39	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Lc	0.27	0/774	0.43	0/1038
33	Ld	0.28	0/903	0.39	0/1216
34	Le	0.31	0/1071	0.40	0/1429
35	Lf	0.31	0/895	0.39	0/1198
36	Lg	0.27	0/916	0.37	0/1220
37	Lh	0.26	0/1023	0.39	0/1351
38	Li	0.24	0/843	0.37	0/1115
39	Lj	0.30	0/720	0.37	0/952
40	Lk	0.22	0/575	0.39	0/761
41	Ll	0.30	0/454	0.39	0/599
42	Lm	0.25	0/435	0.41	0/575
43	Ln	0.26	0/231	0.37	0/294
44	Lo	0.28	0/876	0.38	0/1156
45	Lp	0.28	0/718	0.39	0/953
46	Lr	0.28	0/1017	0.38	0/1364
47	Ls	0.18	0/1519	0.41	0/2052
48	Lt	0.20	0/1009	0.54	0/1363
49	SD	0.18	0/1793	0.39	0/2414
50	SF	0.21	0/1516	0.43	0/2037
51	SK	0.21	0/851	0.50	0/1147
52	SM	0.17	0/950	0.46	0/1275
53	SP	0.20	0/1003	0.44	0/1342
54	SQ	0.21	0/1160	0.48	0/1553
55	SR	0.20	0/1105	0.53	0/1484
56	SS	0.22	0/1216	0.50	0/1628
57	ST	0.18	0/1131	0.39	0/1515
58	SU	0.21	0/831	0.51	0/1115
59	SZ	0.21	0/604	0.45	0/810
60	Sc	0.21	0/508	0.46	0/680
61	Sd	0.22	0/470	0.40	0/623
62	Sf	0.18	0/560	0.51	0/745
63	Sg	0.17	0/2493	0.38	0/3394
64	SA	0.23	0/1778	0.43	0/2416
65	SB	0.23	0/1765	0.39	0/2362
66	SC	0.23	0/1744	0.40	0/2357
67	SE	0.20	0/2118	0.38	0/2849
68	SG	0.19	0/1946	0.40	0/2590
69	SH	0.21	0/1519	0.49	1/2033 (0.0%)
70	SI	0.23	0/1715	0.39	0/2287
71	SJ	0.19	0/1550	0.39	0/2069
72	SL	0.23	0/1268	0.35	0/1696
73	SN	0.22	0/1232	0.34	0/1656
74	SO	0.26	0/1037	0.41	0/1391

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SV	0.21	0/643	0.42	0/860
76	SW	0.25	0/1051	0.40	0/1406
77	SX	0.23	0/1116	0.39	0/1490
78	SY	0.18	0/1083	0.41	0/1438
79	Sa	0.23	0/836	0.36	0/1121
80	Sb	0.22	0/665	0.40	0/891
81	Se	0.17	0/465	0.39	0/612
82	S2	0.25	1/39756 (0.0%)	0.30	0/61939
83	Zt	0.17	0/1779	0.38	0/2771
84	CI	0.16	0/247	0.30	0/323
All	All	0.27	1/231658 (0.0%)	0.35	1/339851 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
61	Sd	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	1383	A2M	O3'-P	5.04	1.61	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	SH	166	VAL	N-CA-C	-5.12	108.84	113.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
61	Sd	12	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Pt	1576	0	803	27	0
2	L5	78444	0	39716	991	0
3	L7	2561	0	1295	20	0
4	L8	3315	0	1685	36	0
5	LA	1898	0	1993	42	0
6	LB	3238	0	3376	78	0
7	LC	2927	0	3104	46	0
8	LD	2382	0	2410	44	0
9	LE	1935	0	2096	37	0
10	LF	1870	0	1996	35	0
11	LG	1927	0	2074	25	0
12	LH	1518	0	1601	25	0
13	LI	1711	0	1749	23	0
14	LJ	1362	0	1399	31	0
15	LL	1701	0	1818	28	0
16	LM	1138	0	1204	24	0
17	LN	1701	0	1749	30	0
18	LO	1650	0	1794	33	0
19	LP	1242	0	1269	17	0
20	LQ	1513	0	1628	25	0
21	LR	1566	0	1729	31	0
22	LS	1453	0	1490	15	0
23	LT	1298	0	1366	19	0
24	LU	825	0	850	46	0
25	LV	979	0	1039	10	0
26	LW	945	0	1003	25	0
27	LX	985	0	1066	18	0
28	LY	1115	0	1205	17	0
29	LZ	1107	0	1182	24	0
30	La	1162	0	1213	13	0
31	Lb	876	0	948	19	0
32	Lc	764	0	804	16	0
33	Ld	888	0	930	18	0
34	Le	1053	0	1147	21	0
35	Lf	876	0	912	14	0
36	Lg	906	0	998	12	0
37	Lh	1015	0	1148	21	0
38	Li	832	0	917	10	0
39	Lj	705	0	737	12	0
40	Lk	569	0	637	13	0
41	Ll	444	0	483	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Lm	429	0	465	7	0
43	Ln	230	0	276	4	0
44	Lo	862	0	929	17	0
45	Lp	708	0	756	13	0
46	Lr	1002	0	1068	21	0
47	Ls	1496	0	1540	46	0
48	Lt	998	0	1032	30	0
49	SD	1765	0	1865	31	0
50	SF	1495	0	1549	42	0
51	SK	827	0	854	35	0
52	SM	940	0	965	28	0
53	SP	985	0	1031	33	0
54	SQ	1142	0	1213	43	0
55	SR	1090	0	1149	30	0
56	SS	1198	0	1261	44	0
57	ST	1112	0	1146	38	0
58	SU	821	0	883	22	0
59	SZ	598	0	656	17	0
60	Sc	506	0	536	11	0
61	Sd	459	0	452	19	0
62	Sf	548	0	551	21	0
63	Sg	2436	0	2393	81	0
64	SA	1741	0	1746	53	0
65	SB	1738	0	1809	53	0
66	SC	1707	0	1791	48	0
67	SE	2076	0	2177	52	0
68	SG	1923	0	2089	58	0
69	SH	1497	0	1590	42	0
70	SI	1686	0	1772	51	0
71	SJ	1525	0	1640	29	0
72	SL	1247	0	1323	26	0
73	SN	1208	0	1294	11	0
74	SO	1024	0	1050	22	0
75	SV	636	0	637	12	0
76	SW	1034	0	1080	25	0
77	SX	1098	0	1167	27	0
78	SY	1065	0	1142	31	0
79	Sa	821	0	870	14	0
80	Sb	651	0	672	22	0
81	Se	459	0	503	13	0
82	S2	36953	0	18679	658	0
83	Zt	1593	0	809	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	CI	247	0	282	37	0
85	L5	179	0	0	0	0
85	L7	3	0	0	0	0
85	L8	5	0	0	0	0
85	LA	1	0	0	0	0
85	LP	1	0	0	0	0
85	LV	1	0	0	0	0
85	Le	1	0	0	0	0
85	S2	26	0	0	0	0
85	SG	1	0	0	0	0
85	SS	1	0	0	0	0
86	L5	98	0	182	8	0
87	L5	100	0	190	3	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
All	All	219971	0	163627	3281	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (3281) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LU:99:TRP:CZ3	84:CI:58:LEU:HB3	1.78	1.17
24:LU:99:TRP:CH2	84:CI:59:GLN:N	2.15	1.14
24:LU:99:TRP:CZ3	84:CI:58:LEU:CB	2.41	1.02
24:LU:99:TRP:HZ3	84:CI:58:LEU:CB	1.72	1.00
83:Zt:26:A:N6	83:Zt:44:G:H1	1.61	0.99
83:Zt:15:G:H22	83:Zt:48:C:H42	1.05	0.97
24:LU:99:TRP:CZ3	84:CI:59:GLN:N	2.34	0.96
24:LU:99:TRP:HH2	84:CI:59:GLN:H	0.95	0.94
82:S2:1748:G:H1	82:S2:1786:U:H3	1.18	0.92
24:LU:116:GLN:O	84:CI:74:LYS:HA	1.70	0.91
83:Zt:26:A:N6	83:Zt:44:G:N1	2.19	0.87
2:L5:1759:G:H1	2:L5:1773:U:H3	1.24	0.86
82:S2:1657:G:H1	82:S2:1667:U:H3	1.24	0.85
2:L5:4946:U:HO2'	35:Lf:2:SER:N	1.74	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:SW:2:VAL:N	82:S2:1091:C:HO2'	1.75	0.84
83:Zt:15:G:N1	83:Zt:48:C:N3	2.24	0.84
83:Zt:26:A:H61	83:Zt:44:G:H1	1.13	0.83
2:L5:4094:G:N2	2:L5:4115:G:OP2	2.12	0.83
83:Zt:15:G:N2	83:Zt:48:C:H42	1.77	0.82
2:L5:512:U:H3	2:L5:647:G:H1	1.26	0.82
24:LU:99:TRP:CE3	84:CI:58:LEU:HD23	2.14	0.81
78:SY:36:PRO:HG3	82:S2:570:C:H4'	1.63	0.81
83:Zt:15:G:H22	83:Zt:48:C:N4	1.79	0.80
21:LR:25:ASP:OD2	84:CI:72:ARG:NH2	2.14	0.80
82:S2:925:G:H1	82:S2:1017:U:H3	1.26	0.79
15:LL:64:VAL:HA	15:LL:67:HIS:HD2	1.45	0.79
2:L5:4093:G:N2	2:L5:4114:C:O2	2.16	0.78
2:L5:2557:G:H1	2:L5:2570:U:H3	0.83	0.78
58:SU:61:LEU:HB2	58:SU:82:MET:HB3	1.66	0.78
74:SO:31:CYS:HB2	74:SO:93:LEU:HD23	1.65	0.78
82:S2:1417:C:H42	82:S2:1422:G:H22	1.28	0.78
82:S2:1776:G:N2	82:S2:1777:G:N7	2.32	0.78
2:L5:1268:G:N7	31:Lb:111:ARG:NH2	2.31	0.78
64:SA:10:MET:HE2	64:SA:55:TRP:HB2	1.66	0.78
54:SQ:49:TYR:O	54:SQ:53:GLU:HB2	1.83	0.78
62:Sf:126:CYS:SG	62:Sf:144:CYS:N	2.56	0.78
47:Ls:160:LEU:HD23	47:Ls:161:ILE:HG23	1.66	0.77
2:L5:1982:G:N2	2:L5:2009:A:O2'	2.18	0.77
2:L5:2520:C:O2	2:L5:2640:G:N2	2.18	0.76
10:LF:243:LEU:O	10:LF:247:MET:HB2	1.84	0.76
67:SE:121:TYR:HB2	67:SE:161:GLN:HE21	1.47	0.76
65:SB:113:MET:HB3	65:SB:142:PHE:HE2	1.50	0.76
24:LU:99:TRP:CZ3	84:CI:58:LEU:CG	2.69	0.76
24:LU:99:TRP:HZ3	84:CI:58:LEU:CG	1.99	0.76
49:SD:105:LEU:HD12	49:SD:122:VAL:HG21	1.67	0.75
68:SG:190:ARG:NH2	82:S2:333:G:N7	2.34	0.75
2:L5:2867:C:H5'	82:S2:368:U:H3	1.51	0.75
57:ST:124:THR:HG23	57:ST:127:GLY:H	1.50	0.75
4:L8:45:C:H4'	41:Ll:11:ARG:HD3	1.69	0.75
2:L5:3688:U:H5''	5:LA:198:ARG:HH22	1.52	0.75
32:Lc:51:ASN:HB2	32:Lc:77:ASN:HB2	1.68	0.75
52:SM:99:LYS:HD3	52:SM:101:ARG:H	1.52	0.75
2:L5:5064:G:H21	19:LP:75:GLN:HE22	1.35	0.75
24:LU:117:ILE:C	84:CI:75:LYS:H	1.95	0.74
70:SI:37:LYS:NZ	70:SI:93:THR:O	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LU:99:TRP:HZ3	84:CI:58:LEU:C	1.94	0.74
57:ST:12:GLN:NE2	82:S2:1593:C:O2	2.20	0.74
50:SF:76:MET:HE3	50:SF:89:THR:HG23	1.68	0.74
6:LB:199:GLU:OE2	6:LB:200:ARG:NH1	2.20	0.74
24:LU:99:TRP:CZ3	84:CI:58:LEU:C	2.64	0.73
48:Lt:107:ASP:OD1	48:Lt:111:ASN:ND2	2.20	0.73
82:S2:1033:G:H1	82:S2:1080:A:HO2'	1.34	0.73
2:L5:2484:A:H62	2:L5:2494:U:H3	1.34	0.73
2:L5:4873:G:N7	18:LO:179:LYS:NZ	2.37	0.73
14:LJ:146:ARG:HG2	14:LJ:147:ARG:HG3	1.70	0.73
63:Sg:152:SER:HG	63:Sg:168:CYS:HG	1.37	0.73
59:SZ:57:LYS:HE3	59:SZ:77:LEU:HD22	1.71	0.72
2:L5:2702:C:OP1	24:LU:101:ARG:NH2	2.21	0.72
50:SF:167:LYS:NZ	50:SF:172:CYS:SG	2.61	0.72
68:SG:152:ASP:OD1	68:SG:155:GLN:NE2	2.23	0.72
2:L5:4242:U:H3	2:L5:4281:A:H2	1.36	0.72
9:LE:240:TYR:OH	9:LE:246:ARG:NH1	2.23	0.72
24:LU:65:ARG:HG2	24:LU:67:LYS:H	1.55	0.72
66:SC:83:LEU:O	75:SV:15:ARG:NH1	2.23	0.72
77:SX:119:ARG:NH2	82:S2:1192:U:OP2	2.23	0.72
78:SY:35:VAL:HG13	78:SY:40:ILE:HD11	1.72	0.71
82:S2:94:G:HO2'	82:S2:508:A:HO2'	1.38	0.71
12:LH:106:GLN:HB2	12:LH:111:LEU:HB3	1.72	0.71
2:L5:3823:G:N2	2:L5:3823:G:OP2	2.23	0.71
58:SU:67:LYS:HG3	58:SU:78:ASP:HB2	1.71	0.71
82:S2:747:U:O2	82:S2:796:G:N2	2.22	0.71
2:L5:1396:G:N7	30:La:110:LYS:NZ	2.37	0.71
2:L5:3949:A:N1	2:L5:4064:C:N4	2.39	0.71
68:SG:22:ARG:HD2	68:SG:25:ARG:HH12	1.55	0.71
2:L5:1366:G:H5''	15:LL:36:ARG:HH12	1.56	0.70
2:L5:1704:C:OP2	10:LF:43:ARG:NH1	2.24	0.70
2:L5:3701:OMC:H5	2:L5:3748:A:H62	1.37	0.70
54:SQ:51:LEU:HD21	54:SQ:81:ILE:HD12	1.73	0.70
82:S2:1417:C:H42	82:S2:1422:G:N2	1.89	0.70
72:SL:82:MET:HE3	72:SL:85:THR:HG23	1.73	0.70
73:SN:71:ILE:HD13	82:S2:1018:U:H5''	1.72	0.70
82:S2:1729:U:H3	82:S2:1805:G:H1	1.37	0.70
75:SV:1:MET:HG2	75:SV:2:GLN:HG2	1.72	0.70
56:SS:85:ASN:OD1	56:SS:97:GLN:NE2	2.24	0.70
2:L5:3937:C:H1'	17:LN:125:SER:HB3	1.72	0.70
21:LR:47:ASP:HB2	84:CI:76:VAL:O	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:84:A:N3	82:S2:150:A:O2'	2.25	0.70
13:LI:87:MET:HG3	13:LI:138:ILE:HG12	1.73	0.70
61:Sd:13:LYS:HE2	82:S2:1556:A:H1'	1.74	0.70
2:L5:2544:G:H1	4:L8:124:U:H5'	1.56	0.70
2:L5:2611:A:H5'	2:L5:2688:G:H4'	1.73	0.70
37:Lh:64:THR:O	37:Lh:68:ASN:ND2	2.25	0.70
82:S2:1417:C:N4	82:S2:1422:G:H22	1.90	0.69
57:ST:126:GLN:HB2	57:ST:129:ARG:HH21	1.58	0.69
2:L5:1095:A:N1	2:L5:1200:G:O6	2.26	0.69
2:L5:3946:G:N2	2:L5:4067:U:O2	2.24	0.69
2:L5:4546:A:N7	5:LA:215:ASN:ND2	2.41	0.69
21:LR:176:ARG:NH2	82:S2:910:G:OP1	2.25	0.69
2:L5:1270:A:H8	2:L5:2106:G:H21	1.40	0.69
49:SD:106:ARG:HG3	49:SD:175:VAL:HG22	1.75	0.69
81:Se:13:ARG:NH1	82:S2:634:A:OP1	2.25	0.69
12:LH:48:LEU:HD11	12:LH:56:ARG:HE	1.58	0.69
9:LE:223:ARG:NH2	9:LE:236:GLU:O	2.25	0.69
82:S2:1277:C:H2'	82:S2:1278:A:H8	1.56	0.68
4:L8:79:G:O2'	37:Lh:46:LYS:NZ	2.25	0.68
62:Sf:107:LYS:NZ	62:Sf:109:ASP:OD1	2.22	0.68
2:L5:2739:C:H4'	45:Lp:52:VAL:HG21	1.75	0.68
5:LA:29:LEU:O	5:LA:123:ARG:NH1	2.25	0.68
12:LH:18:ILE:HG12	12:LH:27:VAL:HG22	1.75	0.68
2:L5:4098:A:H2'	2:L5:4099:G:H4'	1.74	0.68
35:Lf:21:GLN:NE2	35:Lf:23:GLU:OE2	2.27	0.68
83:Zt:48:C:H2'	83:Zt:59:G:H1'	1.74	0.68
82:S2:159:A2M:H2	82:S2:467:G:H21	1.58	0.68
82:S2:1652:G:H1	82:S2:1672:U:H3	1.41	0.68
63:Sg:118:ARG:NH1	63:Sg:134:THR:OG1	2.26	0.68
68:SG:135:PRO:HG2	68:SG:141:ILE:HG22	1.74	0.68
40:Lk:26:LYS:HB2	40:Lk:69:LEU:HD12	1.74	0.68
2:L5:188:G:N2	2:L5:190:G:O6	2.27	0.68
31:Lb:109:ARG:HA	31:Lb:112:ILE:HG12	1.76	0.68
66:SC:200:ARG:O	71:SJ:54:ARG:NH2	2.26	0.68
2:L5:667:A:OP1	46:Lr:67:ARG:NH2	2.26	0.68
82:S2:64:A:N6	82:S2:83:A:OP2	2.27	0.68
24:LU:99:TRP:CZ2	84:CI:59:GLN:HB2	2.29	0.67
49:SD:135:GLU:HB3	49:SD:187:LYS:HB2	1.75	0.67
2:L5:502:C:H3'	2:L5:503:C:H3'	1.76	0.67
47:Ls:68:HIS:O	47:Ls:71:ASN:ND2	2.27	0.67
54:SQ:58:LEU:HB3	54:SQ:62:ARG:HD2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1739:G:N3	2:L5:1742:A:N6	2.41	0.67
32:Lc:20:LEU:O	32:Lc:24:SER:OG	2.11	0.67
63:Sg:152:SER:OG	63:Sg:168:CYS:SG	2.50	0.67
65:SB:26:SER:O	65:SB:51:ARG:NH2	2.27	0.67
82:S2:753:C:N4	82:S2:791:C:O2'	2.27	0.67
82:S2:750:C:H42	82:S2:793:G:H1'	1.59	0.67
2:L5:121:A:OP1	11:LG:110:LYS:NZ	2.27	0.67
2:L5:518:G:H1	2:L5:643:C:H2'	1.58	0.67
74:SO:66:ARG:HG2	82:S2:962:A:H5''	1.77	0.67
2:L5:2601:A:N6	2:L5:2744:A:OP2	2.26	0.67
67:SE:57:THR:OG1	67:SE:60:GLU:OE1	2.10	0.67
56:SS:48:ALA:O	56:SS:66:ARG:NH2	2.28	0.67
82:S2:889:U:OP2	82:S2:896:U:N3	2.27	0.67
82:S2:1536:G:H2'	82:S2:1537:A:H8	1.59	0.67
15:LL:103:ARG:HD2	15:LL:105:LYS:HE3	1.77	0.67
51:SK:3:MET:SD	51:SK:8:ARG:NH2	2.64	0.67
58:SU:19:ARG:NH2	58:SU:93:SER:O	2.28	0.67
66:SC:210:PRO:HB3	66:SC:240:THR:HG21	1.76	0.67
82:S2:1421:A:H5''	82:S2:1422:G:H2'	1.76	0.67
65:SB:103:MET:HG3	65:SB:215:VAL:HG12	1.77	0.66
72:SL:33:LEU:HD12	72:SL:34:PRO:HD2	1.77	0.66
82:S2:928:G:H2'	82:S2:929:G:C8	2.30	0.66
2:L5:2017:A:O2'	2:L5:2018:C:O5'	2.12	0.66
5:LA:114:CYS:HB3	5:LA:165:VAL:HB	1.78	0.66
6:LB:138:GLN:O	6:LB:143:LYS:NZ	2.29	0.66
17:LN:184:ILE:O	17:LN:194:ARG:NH1	2.26	0.66
29:LZ:54:THR:HG22	29:LZ:57:MET:HE3	1.77	0.66
82:S2:165:G:OP2	82:S2:165:G:N2	2.29	0.66
2:L5:180:C:H2'	2:L5:181:C:H6	1.61	0.66
38:Li:2:ALA:N	38:Li:5:TYR:HH	1.93	0.66
69:SH:165:ASN:O	69:SH:169:LYS:NZ	2.28	0.66
2:L5:4525:C:OP1	6:LB:246:ARG:NH2	2.28	0.66
28:LY:67:ILE:O	28:LY:84:ARG:NH2	2.29	0.66
2:L5:4897:G:OP1	16:LM:128:LYS:NZ	2.29	0.66
68:SG:186:GLN:OE1	68:SG:189:ARG:NH2	2.29	0.66
13:LI:188:LYS:HD2	13:LI:212:LEU:HD22	1.78	0.66
55:SR:16:ILE:HD11	55:SR:54:VAL:HG21	1.77	0.66
61:Sd:19:ARG:NH2	82:S2:1661:A:OP1	2.28	0.66
71:SJ:40:LYS:NZ	82:S2:641:A:OP1	2.24	0.66
80:Sb:13:GLU:OE2	80:Sb:17:ARG:NH2	2.28	0.66
82:S2:888:U:H4'	82:S2:889:U:H5'	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:5002:U:OP2	6:LB:385:LYS:NZ	2.29	0.65
65:SB:110:MET:HA	65:SB:113:MET:HE2	1.78	0.65
8:LD:193:GLU:OE2	8:LD:196:ARG:NH2	2.27	0.65
64:SA:80:ARG:NH2	64:SA:165:ASN:O	2.29	0.65
76:SW:107:SER:HB2	82:S2:860:G:H21	1.59	0.65
81:Se:41:ARG:NH2	82:S2:639:C:OP1	2.28	0.65
82:S2:1417:C:N3	82:S2:1422:G:N1	2.43	0.65
16:LM:119:ARG:NH2	18:LO:182:GLU:OE2	2.29	0.65
68:SG:183:ARG:NH2	82:S2:316:G:OP2	2.30	0.65
70:SI:98:LYS:HB3	82:S2:377:G:H5'	1.77	0.65
82:S2:1417:C:O2	82:S2:1422:G:O6	2.14	0.65
2:L5:1996:C:H42	2:L5:2000:G:N2	1.94	0.65
2:L5:2554:U:O2	2:L5:2764:A:N7	2.30	0.65
5:LA:107:MET:HB3	5:LA:111:THR:HG21	1.78	0.65
5:LA:137:ILE:HD11	5:LA:149:LYS:HB2	1.79	0.65
6:LB:10:ARG:NH1	6:LB:11:HIS:O	2.29	0.65
24:LU:99:TRP:CH2	84:CI:59:GLN:HB2	2.31	0.65
66:SC:264:SER:H	66:SC:267:GLN:HE21	1.43	0.65
2:L5:679:C:H2'	2:L5:680:G:H8	1.61	0.65
2:L5:1969:G:H4'	47:Ls:36:GLY:HA2	1.79	0.65
63:Sg:46:THR:H	63:Sg:53:GLY:HA2	1.61	0.65
64:SA:102:ARG:HH12	82:S2:1377:U:H3'	1.62	0.65
67:SE:49:ARG:NH1	82:S2:495:U:OP1	2.30	0.65
2:L5:1996:C:H42	2:L5:2000:G:H22	1.42	0.65
53:SP:37:TYR:O	56:SS:88:LYS:NZ	2.30	0.65
65:SB:144:LYS:HD3	65:SB:208:HIS:HB3	1.79	0.65
2:L5:705:G:OP1	34:Le:5:ARG:NH2	2.30	0.64
26:LW:93:LYS:HA	26:LW:96:GLN:HE22	1.60	0.64
55:SR:133:GLY:HA3	65:SB:152:LYS:HD3	1.77	0.64
58:SU:79:ARG:NH2	82:S2:1669:G:OP1	2.30	0.64
62:Sf:144:CYS:HB2	62:Sf:146:LEU:HD23	1.79	0.64
64:SA:157:VAL:O	75:SV:65:SER:OG	2.16	0.64
26:LW:7:SER:HB2	26:LW:13:ILE:HD11	1.78	0.64
2:L5:1870:C:H2'	2:L5:1871:A2M:H8	1.79	0.64
2:L5:2296:G:O2'	7:LC:242:PRO:O	2.14	0.64
2:L5:4419:U:OP1	2:L5:4475:G:N2	2.31	0.64
2:L5:4473:A:O2'	42:Lm:122:ARG:NH2	2.30	0.64
2:L5:184:U:O2	2:L5:253:G:N2	2.27	0.64
2:L5:3659:G:OP1	5:LA:241:ARG:NH1	2.30	0.64
23:LT:43:LYS:O	23:LT:58:HIS:ND1	2.31	0.64
2:L5:1258:G:H2'	2:L5:1259:G:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3736:A:H2'	2:L5:3737:A:C8	2.32	0.64
47:Ls:192:VAL:HG22	47:Ls:199:TYR:H	1.63	0.64
51:SK:85:LEU:HD21	51:SK:89:ILE:HB	1.79	0.64
68:SG:147:LEU:HD12	68:SG:151:ASP:HB2	1.79	0.64
81:Se:8:ARG:NH1	82:S2:615:C:O3'	2.29	0.64
24:LU:99:TRP:CZ3	84:CI:58:LEU:HG	2.32	0.64
49:SD:161:GLY:HA3	82:S2:1388:A:H61	1.63	0.64
53:SP:25:LEU:HG	53:SP:87:PRO:HB3	1.78	0.64
83:Zt:68:C:H2'	83:Zt:69:G:C8	2.33	0.64
82:S2:482:G:N1	82:S2:485:A:OP2	2.30	0.64
2:L5:1095:A:H2	2:L5:1200:G:H1	1.41	0.64
2:L5:2832:A:OP1	33:Ld:47:LYS:NZ	2.29	0.64
2:L5:4221:C:OP1	86:L5:5263:SPM:N14	2.31	0.64
65:SB:164:ILE:HD12	65:SB:201:CYS:HB3	1.80	0.64
83:Zt:15:G:O6	83:Zt:48:C:O2	2.15	0.64
2:L5:4431:PSU:OP2	13:LI:3:ARG:NH2	2.26	0.64
69:SH:12:ASN:ND2	69:SH:46:THR:O	2.31	0.64
8:LD:271:MET:O	8:LD:276:LYS:NZ	2.30	0.63
18:LO:126:VAL:HG13	18:LO:127:VAL:HG13	1.79	0.63
27:LX:73:HIS:HB3	27:LX:116:LEU:HD23	1.80	0.63
50:SF:127:ARG:HG2	50:SF:136:ARG:HB2	1.80	0.63
61:Sd:44:ARG:NH2	82:S2:1337:4AC:OP1	2.31	0.63
78:SY:34:THR:O	82:S2:570:C:O2'	2.14	0.63
2:L5:1973:G:H4'	48:Lt:117:ARG:HH21	1.63	0.63
2:L5:4413:C:O2	13:LI:158:LYS:NZ	2.30	0.63
63:Sg:87:LEU:HB2	63:Sg:101:PHE:HB2	1.80	0.63
80:Sb:51:GLN:OE1	82:S2:1014:G:N2	2.31	0.63
82:S2:1203:G:H2'	82:S2:1204:A:C8	2.33	0.63
1:Pt:35:A:OP2	54:SQ:146:ARG:NH2	2.32	0.63
2:L5:305:A:OP2	17:LN:15:GLN:NE2	2.30	0.63
2:L5:2845:A:H61	2:L5:3843:C:H42	1.45	0.63
2:L5:3594:C:O2	2:L5:3597:G:N2	2.30	0.63
22:LS:76:LYS:NZ	22:LS:100:LEU:O	2.31	0.63
51:SK:3:MET:SD	82:S2:1314:U:O2'	2.56	0.63
62:Sf:110:GLU:HG2	62:Sf:113:LYS:HD3	1.80	0.63
5:LA:117:GLU:O	5:LA:162:ASN:ND2	2.29	0.63
11:LG:120:LYS:NZ	11:LG:126:GLY:O	2.30	0.63
26:LW:91:MET:O	26:LW:95:ASN:ND2	2.31	0.63
62:Sf:92:LYS:NZ	82:S2:1271:C:OP1	2.32	0.63
71:SJ:107:GLU:O	71:SJ:113:GLN:NE2	2.31	0.63
2:L5:1994:C:H2'	2:L5:1995:G:C8	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2573:A:O2'	29:LZ:112:ARG:NH1	2.32	0.63
48:Lt:114:ARG:NH1	48:Lt:126:SER:O	2.30	0.63
51:SK:11:ILE:HD11	51:SK:21:MET:HE3	1.80	0.63
55:SR:17:ILE:HD11	55:SR:54:VAL:HG13	1.80	0.63
2:L5:513:U:N3	2:L5:516:C:OP2	2.30	0.63
52:SM:113:ASP:OD1	52:SM:114:TYR:N	2.32	0.63
83:Zt:68:C:H2'	83:Zt:69:G:H8	1.64	0.63
1:Pt:50:U:H3	1:Pt:64:G:H1	0.75	0.63
2:L5:180:C:H2'	2:L5:181:C:C6	2.33	0.63
19:LP:138:PRO:HB3	19:LP:140:MET:HE3	1.80	0.63
47:Ls:53:VAL:HA	47:Ls:89:VAL:HA	1.80	0.63
2:L5:512:U:O4	2:L5:647:G:O6	2.17	0.63
2:L5:664:G:N2	2:L5:666:G:O6	2.32	0.63
2:L5:1704:C:O3'	10:LF:46:ARG:NH1	2.31	0.63
2:L5:3717:A:H2'	2:L5:3718:A2M:H8	1.81	0.63
2:L5:4742:G:H2'	2:L5:4743:G:H8	1.62	0.63
56:SS:22:GLY:HA2	56:SS:56:ALA:HB3	1.78	0.63
82:S2:508:A:H3'	82:S2:509:OMG:H8	1.62	0.63
2:L5:4742:G:OP1	2:L5:4900:C:N4	2.32	0.62
10:LF:96:ARG:HH12	10:LF:224:THR:HG22	1.64	0.62
25:LV:43:LYS:HG3	25:LV:60:MET:HE3	1.80	0.62
2:L5:456:C:N4	2:L5:701:G:O6	2.32	0.62
63:Sg:164:ILE:HG22	63:Sg:178:ASN:HA	1.81	0.62
76:SW:3:ARG:HH22	76:SW:28:ARG:HH21	1.47	0.62
2:L5:1100:U:O3'	2:L5:1167:C:N4	2.31	0.62
9:LE:141:ARG:NH1	9:LE:191:GLN:O	2.32	0.62
24:LU:72:VAL:HG21	24:LU:83:LEU:HD11	1.81	0.62
38:Li:67:LYS:HG2	38:Li:71:LYS:HE2	1.81	0.62
82:S2:1829:G:H1'	82:S2:1850:MA6:H2	1.80	0.62
2:L5:1414:C:H2'	2:L5:1415:G:H8	1.63	0.62
2:L5:3946:G:H1	2:L5:4067:U:H3	1.48	0.62
4:L8:52:A:H5'	41:Ll:21:ARG:HD3	1.82	0.62
78:SY:7:ILE:HG12	78:SY:27:VAL:HG12	1.82	0.62
2:L5:135:G:H22	37:Lh:94:ARG:HG3	1.64	0.62
2:L5:989:U:O2	2:L5:1064:G:N2	2.31	0.62
57:ST:129:ARG:HH11	57:ST:133:ARG:HH22	1.46	0.62
66:SC:123:ARG:NH2	82:S2:1358:U:OP2	2.33	0.62
2:L5:3697:U:H5''	2:L5:3698:G:H5'	1.81	0.62
66:SC:168:GLY:N	66:SC:179:THR:O	2.30	0.62
82:S2:145:G:H2'	82:S2:146:G:C8	2.34	0.62
2:L5:1932:A:OP1	18:LO:49:ARG:NH2	2.28	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Sg:205:SER:HA	63:Sg:221:LEU:HB2	1.80	0.62
2:L5:88:A:N7	20:LQ:173:LYS:NZ	2.47	0.62
2:L5:1332:C:H2'	2:L5:1333:A:H8	1.62	0.62
2:L5:2557:G:O6	2:L5:2570:U:O4	2.16	0.62
47:Ls:7:ALA:HA	47:Ls:10:LYS:HE3	1.82	0.62
66:SC:193:VAL:HG11	66:SC:240:THR:HG22	1.82	0.62
82:S2:1536:G:H2'	82:S2:1537:A:C8	2.35	0.62
2:L5:102:G:HO2'	2:L5:1381:U:HO2'	1.47	0.62
2:L5:2859:G:H21	2:L5:3837:C:H1'	1.64	0.62
2:L5:4251:A:H5''	14:LJ:108:GLY:HA3	1.82	0.62
2:L5:4859:C:H2'	2:L5:4860:G:C8	2.34	0.62
59:SZ:80:ARG:O	82:S2:1598:G:O2'	2.15	0.62
78:SY:98:GLU:O	78:SY:101:LYS:NZ	2.33	0.62
2:L5:1646:A:O2'	39:Lj:49:TRP:O	2.17	0.61
31:Lb:65:MET:HG2	31:Lb:68:ARG:HH12	1.65	0.61
78:SY:37:LYS:HA	78:SY:40:ILE:HD12	1.81	0.61
44:Lo:2:VAL:N	44:Lo:90:HIS:O	2.33	0.61
63:Sg:63:SER:HB2	82:S2:1398:G:H1'	1.82	0.61
67:SE:161:GLN:OE1	67:SE:170:THR:OG1	2.13	0.61
69:SH:78:ARG:NH1	69:SH:82:GLU:OE2	2.30	0.61
82:S2:1226:G:N1	82:S2:1639:G7M:OP2	2.26	0.61
82:S2:1228:A:H2'	82:S2:1229:G:C8	2.35	0.61
11:LG:52:THR:HG22	27:LX:41:ARG:HG3	1.81	0.61
48:Lt:22:VAL:O	48:Lt:48:LYS:NZ	2.24	0.61
68:SG:186:GLN:NE2	82:S2:332:G:O6	2.32	0.61
2:L5:1982:G:H2'	2:L5:1983:A:O4'	2.01	0.61
2:L5:3681:G:N1	5:LA:118:GLU:OE2	2.34	0.61
2:L5:4774:C:O2'	2:L5:4775:C:O2	2.12	0.61
1:Pt:50:U:O2	1:Pt:64:G:N2	2.22	0.61
2:L5:67:C:OP2	2:L5:312:G:N2	2.32	0.61
2:L5:2018:C:H2'	2:L5:2019:C:H6	1.66	0.61
2:L5:4541:G:N2	2:L5:4544:A:OP2	2.28	0.61
21:LR:151:ARG:HH21	72:SL:118:ARG:HD3	1.66	0.61
43:Ln:8:LYS:NZ	82:S2:1846:G:N7	2.47	0.61
50:SF:134:VAL:HG12	50:SF:135:ARG:HG2	1.82	0.61
57:ST:11:GLN:HB2	82:S2:1542:C:H4'	1.83	0.61
66:SC:211:LYS:HG2	66:SC:215:MET:HE2	1.81	0.61
2:L5:1655:C:OP2	30:La:26:ARG:NH1	2.34	0.61
7:LC:218:ILE:HA	7:LC:229:LEU:HD13	1.82	0.61
20:LQ:154:LYS:NZ	20:LQ:159:PRO:O	2.29	0.61
2:L5:500:G:N2	2:L5:504:G:O2'	2.23	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1998:A:O2'	2:L5:2019:C:O2'	2.18	0.61
2:L5:4414:A:O2'	2:L5:4427:G:N2	2.29	0.61
2:L5:4594:U:H2'	2:L5:4595:G:H8	1.65	0.61
6:LB:14:LEU:HD22	6:LB:17:LEU:HD11	1.83	0.61
9:LE:165:LEU:HD11	9:LE:176:THR:HG22	1.81	0.61
57:ST:121:ARG:HH21	82:S2:1563:G:H5''	1.66	0.61
67:SE:71:LYS:HB3	67:SE:91:SER:HB2	1.82	0.61
70:SI:116:HIS:O	70:SI:152:ARG:NH2	2.30	0.61
82:S2:1228:A:H2'	82:S2:1229:G:H8	1.65	0.61
64:SA:42:LYS:HE3	64:SA:48:ILE:HD11	1.82	0.61
80:Sb:36:LYS:HE3	80:Sb:80:ARG:HH21	1.66	0.61
18:LO:34:VAL:HG22	18:LO:103:LYS:HB2	1.82	0.61
25:LV:35:LYS:HB2	25:LV:67:LYS:HG3	1.82	0.61
46:Lr:103:ARG:HH21	46:Lr:106:LEU:HD11	1.66	0.61
53:SP:44:ARG:NE	53:SP:44:ARG:O	2.34	0.61
82:S2:368:U:H3'	82:S2:369:C:H2'	1.82	0.61
2:L5:262:G:H2'	2:L5:263:G:H8	1.66	0.61
17:LN:164:LEU:O	17:LN:169:ARG:NH2	2.33	0.61
13:LI:14:ASN:O	13:LI:128:ARG:NH2	2.23	0.60
2:L5:982:U:OP1	9:LE:73:TYR:OH	2.15	0.60
2:L5:1702:C:H4'	7:LC:308:LYS:HD2	1.83	0.60
41:LI:28:ARG:HA	41:LI:33:ASN:HD22	1.65	0.60
50:SF:168:THR:N	50:SF:171:GLU:OE2	2.33	0.60
82:S2:647:U:H2'	82:S2:648:A:H8	1.66	0.60
2:L5:1351:G:O6	20:LQ:55:ARG:NH1	2.34	0.60
2:L5:2407:G:O6	41:LI:2:SER:N	2.35	0.60
56:SS:5:ILE:N	59:SZ:50:PHE:O	2.34	0.60
2:L5:1503:A:H4'	2:L5:1504:G:H5'	1.82	0.60
2:L5:1573:G:OP1	21:LR:92:LYS:NZ	2.30	0.60
2:L5:4088:C:OP1	5:LA:37:ARG:NH1	2.35	0.60
8:LD:265:ARG:NH1	8:LD:267:ASN:O	2.32	0.60
20:LQ:122:THR:OG1	20:LQ:125:GLN:OE1	2.16	0.60
24:LU:99:TRP:HZ3	84:CI:58:LEU:HG	1.64	0.60
31:Lb:56:LYS:O	31:Lb:60:ASN:ND2	2.34	0.60
56:SS:15:VAL:HG12	56:SS:16:LEU:HG	1.84	0.60
78:SY:119:GLY:HA2	82:S2:85:A:H5'	1.83	0.60
82:S2:857:U:H2'	82:S2:858:A:H8	1.65	0.60
2:L5:907:C:H2'	2:L5:908:G:H8	1.66	0.60
7:LC:254:GLU:OE2	7:LC:258:ARG:NE	2.34	0.60
9:LE:161:ARG:NH1	9:LE:273:SER:OG	2.34	0.60
53:SP:130:ARG:HD3	53:SP:131:PRO:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1560:U:HO2'	82:S2:1583:C:HO2'	1.47	0.60
2:L5:1942:A:H2'	2:L5:1943:A:C8	2.37	0.60
2:L5:2460:A:OP2	87:L5:5293:SPD:N10	2.34	0.60
3:L7:7:G:OP1	8:LD:33:ARG:NH1	2.34	0.60
65:SB:186:ASN:HA	65:SB:189:ILE:HD12	1.82	0.60
81:Se:34:ARG:NH2	82:S2:642:U:OP2	2.35	0.60
82:S2:588:G:OP2	82:S2:588:G:N2	2.35	0.60
2:L5:137:G:H2'	2:L5:138:G:H8	1.66	0.60
2:L5:4472:G:O2'	42:Lm:100:TYR:O	2.19	0.60
33:Ld:24:GLU:OE2	33:Ld:87:ARG:NH2	2.28	0.60
48:Lt:107:ASP:O	48:Lt:111:ASN:ND2	2.35	0.60
83:Zt:15:G:C6	83:Zt:48:C:O2	2.54	0.60
2:L5:1326:A2M:H2'	2:L5:1327:C:C6	2.36	0.60
10:LF:238:ASP:O	10:LF:241:ASN:ND2	2.35	0.60
63:Sg:176:VAL:HG23	63:Sg:185:LYS:HB2	1.84	0.60
70:SI:143:LYS:NZ	82:S2:202:G:OP1	2.35	0.60
45:Lp:37:TYR:HD2	45:Lp:71:TYR:HB2	1.67	0.60
63:Sg:18:VAL:HG21	63:Sg:307:VAL:HB	1.83	0.60
77:SX:105:PHE:HD1	77:SX:121:LYS:HB3	1.67	0.60
6:LB:147:GLU:OE2	6:LB:198:ARG:NH2	2.35	0.60
21:LR:49:LEU:HD21	84:CI:75:LYS:HG3	1.83	0.60
48:Lt:65:GLN:HG3	48:Lt:67:ARG:H	1.67	0.60
64:SA:118:GLU:HG3	66:SC:65:LYS:HE2	1.83	0.60
68:SG:3:LEU:HD13	68:SG:109:LEU:HB3	1.84	0.60
73:SN:2:GLY:N	82:S2:923:G:OP1	2.35	0.60
75:SV:42:VAL:HG23	75:SV:43:THR:HG23	1.84	0.60
82:S2:981:A:H2'	82:S2:982:G:C8	2.36	0.60
82:S2:1656:G:H1	82:S2:1668:U:H3	1.48	0.60
2:L5:1480:C:O2'	2:L5:1482:G:OP2	2.20	0.59
6:LB:10:ARG:NH2	6:LB:265:SER:O	2.35	0.59
63:Sg:107:ASP:HB2	63:Sg:125:ARG:HG3	1.84	0.59
66:SC:169:TYR:OH	66:SC:175:GLY:O	2.18	0.59
67:SE:153:LEU:O	67:SE:174:LYS:NZ	2.34	0.59
78:SY:11:LYS:HB2	78:SY:24:VAL:HG22	1.84	0.59
82:S2:1581:C:H5'	82:S2:1582:C:H5	1.67	0.59
2:L5:4670:C:O2'	2:L5:4672:A:OP2	2.19	0.59
65:SB:34:LYS:NZ	65:SB:43:ASN:OD1	2.32	0.59
65:SB:168:MET:HA	65:SB:171:ILE:HG22	1.84	0.59
2:L5:2579:G:N2	2:L5:2582:A:OP2	2.28	0.59
12:LH:113:GLU:OE2	12:LH:125:ARG:NH1	2.34	0.59
64:SA:49:ILE:HD11	64:SA:150:THR:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SG:72:ARG:NH2	82:S2:466:G:O2'	2.35	0.59
68:SG:92:ARG:O	82:S2:453:C:O2'	2.16	0.59
69:SH:51:ILE:HD11	69:SH:176:VAL:HG12	1.83	0.59
71:SJ:111:GLN:OE1	71:SJ:127:ARG:NH1	2.35	0.59
2:L5:261:G:H2'	2:L5:262:G:C8	2.37	0.59
6:LB:292:LEU:HB2	6:LB:298:LEU:HD12	1.84	0.59
28:LY:30:MET:HE1	28:LY:75:ARG:HG2	1.84	0.59
63:Sg:6:THR:N	63:Sg:311:GLN:O	2.36	0.59
82:S2:1528:G:O2'	82:S2:1666:C:OP1	2.19	0.59
2:L5:1408:G:O2'	2:L5:1411:C:N4	2.33	0.59
2:L5:2577:C:OP1	29:LZ:111:ARG:NH2	2.36	0.59
28:LY:110:LYS:O	28:LY:115:ARG:NH1	2.35	0.59
33:Ld:64:ILE:HG23	33:Ld:68:LEU:HD23	1.85	0.59
70:SI:76:THR:HG21	70:SI:104:ILE:HD12	1.85	0.59
77:SX:68:LYS:HB3	77:SX:91:LEU:HD13	1.85	0.59
2:L5:2092:G:O2'	2:L5:2262:G:N2	2.35	0.59
2:L5:4238:G:H2'	2:L5:4239:A:H8	1.67	0.59
2:L5:4743:G:H2'	2:L5:4744:A:C8	2.36	0.59
66:SC:81:ILE:HG21	66:SC:88:ILE:HD11	1.84	0.59
2:L5:1516:G:O2'	15:LL:18:TRP:NE1	2.36	0.59
2:L5:1669:A:OP1	31:Lb:18:ARG:NH2	2.36	0.59
2:L5:1961:G:N2	2:L5:2024:G:O2'	2.34	0.59
2:L5:2284:G:OP1	30:La:7:LYS:NZ	2.35	0.59
2:L5:3688:U:H5''	5:LA:198:ARG:NH2	2.17	0.59
53:SP:81:ARG:NH1	53:SP:120:SER:OG	2.35	0.59
71:SJ:83:ARG:HG2	71:SJ:150:ARG:HD3	1.84	0.59
2:L5:1756:U:O2'	2:L5:1758:G:OP2	2.18	0.59
2:L5:2716:C:O3'	24:LU:107:LYS:NZ	2.36	0.59
2:L5:4471:PSU:OP1	12:LH:168:LYS:NZ	2.36	0.59
2:L5:4570:G:H2'	2:L5:4571:A2M:H8	1.85	0.59
7:LC:209:ILE:HB	7:LC:229:LEU:HD23	1.85	0.59
9:LE:179:LEU:HD12	9:LE:183:ARG:HA	1.85	0.59
13:LI:36:LEU:HD11	13:LI:69:ARG:HD2	1.84	0.59
63:Sg:8:ARG:HB3	63:Sg:309:VAL:HG13	1.85	0.59
69:SH:144:ILE:HB	76:SW:52:ILE:HB	1.85	0.59
82:S2:1372:U:OP1	82:S2:1385:G:N2	2.26	0.59
2:L5:709:C:OP1	35:Lf:89:ARG:NH2	2.35	0.59
2:L5:2458:C:H5''	17:LN:67:ARG:HD2	1.83	0.59
2:L5:3641:U:OP2	2:L5:3646:A:N6	2.36	0.59
2:L5:4612:C:C2	12:LH:120:GLU:HB2	2.38	0.58
27:LX:86:ALA:O	27:LX:90:ILE:HD12	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SF:34:SER:HA	60:Sc:55:VAL:HG23	1.85	0.58
50:SF:76:MET:SD	82:S2:1535:U:N3	2.76	0.58
50:SF:127:ARG:HG2	50:SF:136:ARG:HE	1.68	0.58
71:SJ:38:ARG:N	71:SJ:42:GLU:OE2	2.27	0.58
82:S2:1243:U:OP2	82:S2:1518:C:O2'	2.16	0.58
2:L5:1100:U:H1'	2:L5:1167:C:H42	1.68	0.58
4:L8:60:G:OP1	27:LX:68:ARG:NH2	2.36	0.58
47:Ls:116:ILE:HG23	47:Ls:118:PRO:HD3	1.85	0.58
62:Sf:138:ARG:NE	82:S2:1292:C:O2	2.35	0.58
80:Sb:67:THR:OG1	80:Sb:70:LYS:O	2.17	0.58
2:L5:500:G:OP1	2:L5:504:G:N2	2.36	0.58
2:L5:3611:A:H2	2:L5:5016:A:H8	1.50	0.58
2:L5:4617:G:OP1	6:LB:62:ARG:NH1	2.36	0.58
22:LS:5:GLY:O	22:LS:111:ARG:NH2	2.36	0.58
58:SU:85:HIS:ND1	82:S2:1447:G:OP1	2.36	0.58
2:L5:1866:U:OP1	13:LI:4:ARG:NH1	2.35	0.58
2:L5:3732:A:H2'	2:L5:3733:A:H8	1.68	0.58
47:Ls:45:MET:HE1	48:Lt:122:ALA:HA	1.85	0.58
55:SR:104:GLU:OE1	64:SA:39:TYR:OH	2.18	0.58
63:Sg:252:THR:HG21	63:Sg:257:LYS:HD2	1.83	0.58
67:SE:61:VAL:HG13	67:SE:80:ILE:HD11	1.84	0.58
2:L5:2543:A:H2	2:L5:2773:G:H22	1.49	0.58
2:L5:2658:G:N2	2:L5:2676:A:OP2	2.36	0.58
2:L5:3867:A2M:H8	2:L5:3867:A2M:H5''	1.86	0.58
50:SF:167:LYS:HA	59:SZ:71:ALA:HB1	1.84	0.58
52:SM:37:GLU:HA	52:SM:40:LYS:HG2	1.86	0.58
68:SG:11:GLY:HA2	82:S2:166:A2M:HM'1	1.86	0.58
2:L5:4149:C:OP1	29:LZ:59:LYS:N	2.36	0.58
4:L8:8:U:H2'	4:L8:9:A:C8	2.39	0.58
33:Ld:93:ASN:ND2	33:Ld:100:ASN:O	2.35	0.58
34:Le:90:MET:HE1	46:Lr:113:ARG:HA	1.85	0.58
2:L5:262:G:H2'	2:L5:263:G:C8	2.39	0.58
2:L5:989:U:H3	2:L5:1064:G:H1	1.50	0.58
2:L5:4064:C:H2'	2:L5:4065:G:C8	2.38	0.58
82:S2:1354:G:N2	82:S2:1357:A:OP2	2.33	0.58
83:Zt:26:A:N6	83:Zt:44:G:C6	2.70	0.58
2:L5:2017:A:O2'	2:L5:2018:C:H6	1.85	0.58
63:Sg:207:CYS:HB3	63:Sg:221:LEU:HD21	1.86	0.58
82:S2:28:U:H2'	82:S2:29:G:H8	1.69	0.58
1:Pt:38:C:O2'	82:S2:1058:A:OP1	2.22	0.58
2:L5:62:A:N3	2:L5:77:U:O2'	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1095:A:C2	2:L5:1200:G:N1	2.70	0.58
2:L5:1985:G:N2	2:L5:2003:G:O2'	2.36	0.58
2:L5:2898:G:OP2	21:LR:135:LYS:NZ	2.33	0.58
2:L5:4728:U:OP1	6:LB:132:LYS:NZ	2.35	0.58
15:LL:153:PRO:HG2	15:LL:156:PRO:HB3	1.86	0.58
21:LR:172:ARG:NH1	82:S2:909:G:OP1	2.36	0.58
50:SF:164:ARG:NH1	82:S2:1533:A:OP2	2.37	0.58
58:SU:80:PHE:HB3	61:Sd:52:PHE:HB3	1.85	0.58
66:SC:77:SER:OG	66:SC:79:GLU:OE1	2.22	0.58
67:SE:80:ILE:HG23	67:SE:81:THR:HG23	1.85	0.58
67:SE:192:ILE:HG12	67:SE:243:GLY:HA3	1.85	0.58
82:S2:795:A:H2'	82:S2:796:G:C8	2.39	0.58
2:L5:4373:G:N7	44:Lo:61:LYS:NZ	2.50	0.58
11:LG:120:LYS:NZ	11:LG:127:ASP:O	2.36	0.58
21:LR:173:ARG:O	21:LR:176:ARG:NH1	2.37	0.58
54:SQ:89:SER:OG	54:SQ:119:LEU:O	2.19	0.58
63:Sg:166:VAL:HG12	63:Sg:176:VAL:HG12	1.85	0.58
64:SA:10:MET:HE1	64:SA:18:PHE:HE2	1.69	0.58
64:SA:22:GLY:O	64:SA:24:HIS:ND1	2.37	0.58
68:SG:183:ARG:HH22	82:S2:316:G:H5''	1.69	0.58
70:SI:65:PHE:HD2	70:SI:104:ILE:HD13	1.68	0.58
71:SJ:38:ARG:O	81:Se:34:ARG:NH1	2.37	0.58
75:SV:30:ALA:O	75:SV:60:ARG:NH1	2.37	0.58
2:L5:4274:A:H2'	2:L5:4275:G:C8	2.38	0.57
4:L8:75:OMG:OP2	28:LY:74:TYR:OH	2.22	0.57
29:LZ:9:LYS:NZ	29:LZ:83:THR:O	2.32	0.57
29:LZ:14:LEU:HD21	29:LZ:81:MET:HB2	1.85	0.57
35:Lf:50:VAL:HG22	35:Lf:69:VAL:HG12	1.84	0.57
2:L5:665:C:H4'	2:L5:666:G:H5'	1.86	0.57
2:L5:2587:A:OP2	36:Lg:70:THR:OG1	2.19	0.57
2:L5:4441:A:H5''	13:LI:114:GLY:HA2	1.85	0.57
3:L7:54:A:O4'	14:LJ:10:ASN:ND2	2.37	0.57
30:La:72:THR:HG22	30:La:110:LYS:HB3	1.86	0.57
50:SF:185:SER:H	50:SF:190:ILE:HD11	1.69	0.57
50:SF:195:GLU:HA	50:SF:198:ARG:HG2	1.86	0.57
77:SX:107:ARG:HG3	77:SX:110:HIS:HB3	1.85	0.57
82:S2:1129:G:H3'	82:S2:1130:G:H21	1.69	0.57
2:L5:158:A:N1	2:L5:276:C:O2'	2.29	0.57
2:L5:1942:A:H2'	2:L5:1943:A:H8	1.69	0.57
10:LF:171:ASP:OD1	10:LF:172:ASN:N	2.36	0.57
50:SF:127:ARG:H	50:SF:135:ARG:HD2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1277:C:H2'	82:S2:1278:A:C8	2.37	0.57
2:L5:268:G:H2'	2:L5:269:G:H8	1.69	0.57
2:L5:495:C:H2'	2:L5:496:G:C8	2.39	0.57
2:L5:1558:A:H2'	2:L5:1559:G:H8	1.69	0.57
44:Lo:71:GLU:OE2	44:Lo:78:ARG:NH2	2.37	0.57
48:Lt:12:VAL:HG11	48:Lt:64:ILE:HA	1.86	0.57
48:Lt:121:LEU:HD13	48:Lt:129:ILE:HG13	1.87	0.57
54:SQ:139:ALA:HB2	82:S2:1650:A:H5''	1.86	0.57
82:S2:1777:G:H2'	82:S2:1778:C:H6	1.68	0.57
3:L7:61:G:H5''	8:LD:271:MET:HE2	1.87	0.57
57:ST:13:GLU:HA	57:ST:16:ARG:HE	1.69	0.57
66:SC:207:ALA:HB2	82:S2:4:C:H4'	1.86	0.57
71:SJ:137:VAL:HG22	71:SJ:157:ILE:HG22	1.87	0.57
2:L5:3717:A:H2'	2:L5:3718:A2M:C8	2.34	0.57
5:LA:140:ASN:ND2	5:LA:143:THR:OG1	2.38	0.57
8:LD:278:ASP:O	8:LD:282:GLN:HG3	2.04	0.57
22:LS:96:GLU:OE2	22:LS:139:ARG:N	2.36	0.57
56:SS:6:PRO:HD2	56:SS:9:PHE:HB2	1.85	0.57
2:L5:173:C:O2'	37:Lh:111:GLU:OE1	2.22	0.57
2:L5:460:C:H2'	2:L5:461:G:H8	1.70	0.57
2:L5:1207:C:H2'	2:L5:1208:G:H8	1.69	0.57
6:LB:299:ILE:HB	6:LB:313:SER:HB3	1.86	0.57
14:LJ:78:LYS:HE3	14:LJ:82:ILE:HD11	1.86	0.57
63:Sg:247:TRP:HB3	63:Sg:258:ILE:HD11	1.87	0.57
2:L5:4954:G:H2'	2:L5:4955:A:H8	1.70	0.57
5:LA:198:ARG:NH1	5:LA:199:VAL:O	2.37	0.57
8:LD:62:CYS:HB3	8:LD:105:LEU:HD22	1.86	0.57
12:LH:95:VAL:HG12	42:Lm:82:LEU:HD13	1.86	0.57
50:SF:161:ALA:O	50:SF:165:ASN:ND2	2.36	0.57
56:SS:46:ARG:NH1	57:ST:50:GLU:OE2	2.38	0.57
68:SG:136:LYS:NZ	68:SG:175:LYS:O	2.27	0.57
83:Zt:30:G:H2'	83:Zt:31:A:H8	1.69	0.57
2:L5:3589:G:N2	2:L5:3590:G:O6	2.38	0.57
2:L5:4238:G:H2'	2:L5:4239:A:C8	2.39	0.57
14:LJ:38:LYS:HA	14:LJ:41:GLU:HG2	1.87	0.57
28:LY:31:SER:HA	28:LY:48:PRO:HA	1.87	0.57
50:SF:40:ALA:HB3	50:SF:67:PRO:HA	1.86	0.57
66:SC:209:VAL:HG11	66:SC:233:LEU:HD11	1.87	0.57
2:L5:308:G:OP2	2:L5:308:G:N2	2.32	0.57
16:LM:47:ARG:HD2	22:LS:73:LEU:HD23	1.87	0.57
35:Lf:43:LEU:O	35:Lf:109:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SK:90:VAL:HB	51:SK:94:LEU:HD23	1.86	0.57
54:SQ:76:GLY:O	82:S2:1544:C:O2'	2.22	0.57
63:Sg:283:PRO:O	63:Sg:285:GLN:NE2	2.38	0.57
67:SE:87:MET:HG3	67:SE:100:ARG:HD2	1.87	0.57
72:SL:35:ARG:NH2	72:SL:55:TYR:O	2.38	0.57
2:L5:386:A:O2'	28:LY:87:ARG:NH1	2.38	0.56
2:L5:2295:C:O2'	7:LC:45:ARG:NH2	2.38	0.56
6:LB:46:PHE:HE2	6:LB:81:THR:HB	1.69	0.56
47:Ls:28:PHE:HD2	47:Ls:189:ILE:HG21	1.70	0.56
62:Sf:95:ARG:HH12	82:S2:1291:A:H62	1.53	0.56
71:SJ:121:LYS:NZ	82:S2:527:C:O2'	2.28	0.56
82:S2:159:A2M:O5'	82:S2:159:A2M:H8	2.05	0.56
2:L5:422:C:H2'	2:L5:423:G:H8	1.70	0.56
47:Ls:148:SER:O	47:Ls:151:THR:OG1	2.22	0.56
56:SS:75:ARG:NH1	56:SS:81:ASP:OD1	2.37	0.56
63:Sg:45:LEU:O	63:Sg:47:ARG:NH1	2.38	0.56
63:Sg:57:ARG:NH2	63:Sg:94:THR:O	2.38	0.56
64:SA:200:ASP:HA	64:SA:203:PHE:CD2	2.40	0.56
68:SG:3:LEU:HD12	68:SG:111:LEU:HD11	1.87	0.56
68:SG:190:ARG:HH12	82:S2:334:C:H5	1.53	0.56
68:SG:198:ARG:NH1	82:S2:126:G:OP2	2.38	0.56
78:SY:21:LYS:HE2	78:SY:75:ILE:HD11	1.87	0.56
2:L5:919:C:OP1	16:LM:69:HIS:ND1	2.28	0.56
2:L5:1802:A:N3	23:LT:130:ARG:NH2	2.53	0.56
2:L5:2362:U:H2'	2:L5:2363:A2M:H8	1.88	0.56
2:L5:4247:G:H5'	8:LD:4:VAL:HG11	1.88	0.56
2:L5:4474:A:OP2	2:L5:4476:C:N4	2.38	0.56
13:LI:3:ARG:NH1	13:LI:63:GLU:OE2	2.38	0.56
17:LN:104:GLU:OE2	17:LN:108:ARG:NH2	2.37	0.56
48:Lt:81:ILE:HD13	48:Lt:113:ALA:HB1	1.88	0.56
53:SP:57:LEU:HD21	53:SP:86:LEU:HD22	1.87	0.56
54:SQ:140:ARG:HB2	82:S2:1644:C:H4'	1.87	0.56
74:SO:104:ARG:NH2	82:S2:959:G:OP1	2.37	0.56
80:Sb:23:ARG:NH1	80:Sb:27:SER:O	2.39	0.56
82:S2:15:U:O2'	82:S2:669:A:N6	2.37	0.56
2:L5:75:G:O6	15:LL:103:ARG:NH1	2.39	0.56
2:L5:1499:C:OP1	20:LQ:150:ARG:NH2	2.38	0.56
2:L5:2583:C:OP2	36:Lg:76:ARG:NH1	2.35	0.56
2:L5:2846:G:OP1	25:LV:85:ARG:NH2	2.38	0.56
2:L5:4910:G:H22	18:LO:107:GLY:HA3	1.70	0.56
50:SF:84:GLY:O	82:S2:1673:U:O2'	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SM:20:GLU:HG2	52:SM:119:GLN:HB2	1.86	0.56
60:Sc:33:GLU:HG3	60:Sc:41:SER:HB3	1.86	0.56
70:SI:44:HIS:ND1	82:S2:1740:C:OP1	2.32	0.56
82:S2:1759:G:N2	82:S2:1760:G:O6	2.38	0.56
82:S2:1773:C:H2'	82:S2:1774:C:H5''	1.88	0.56
83:Zt:9:A:O2'	83:Zt:45:G:N3	2.33	0.56
2:L5:152:U:OP2	17:LN:49:ARG:NH2	2.30	0.56
2:L5:2517:A:H5'	36:Lg:62:LYS:HD3	1.87	0.56
2:L5:4128:A:O2'	11:LG:33:GLU:O	2.19	0.56
2:L5:4742:G:H2'	2:L5:4743:G:C8	2.41	0.56
29:LZ:11:VAL:HG12	29:LZ:82:PRO:HA	1.86	0.56
29:LZ:46:ILE:HA	29:LZ:70:SER:HA	1.87	0.56
48:Lt:117:ARG:HD3	48:Lt:119:ARG:H	1.70	0.56
50:SF:60:ARG:NH2	82:S2:1679:A:OP1	2.38	0.56
71:SJ:164:PRO:HB3	71:SJ:170:PRO:HA	1.88	0.56
80:Sb:11:SER:OG	80:Sb:14:GLU:OE1	2.22	0.56
82:S2:639:C:H2'	82:S2:640:A:H8	1.70	0.56
6:LB:222:VAL:O	6:LB:343:ARG:NH1	2.39	0.56
7:LC:116:ASN:HB2	7:LC:119:GLN:HG3	1.88	0.56
39:Lj:2:THR:HG22	39:Lj:4:GLY:H	1.71	0.56
68:SG:5:ILE:HD12	68:SG:124:LEU:HD22	1.87	0.56
69:SH:36:LEU:HD11	69:SH:78:ARG:HG2	1.88	0.56
82:S2:543:C:H3'	82:S2:544:G:H8	1.71	0.56
2:L5:4473:A:OP1	42:Lm:124:LYS:NZ	2.35	0.56
2:L5:4620:OMU:OP2	2:L5:4670:C:N4	2.26	0.56
26:LW:56:ARG:HH21	26:LW:61:LYS:HB3	1.70	0.56
32:Lc:30:GLY:O	32:Lc:34:THR:OG1	2.19	0.56
52:SM:128:PHE:HD1	52:SM:131:LYS:HZ3	1.53	0.56
54:SQ:72:VAL:HG21	54:SQ:84:ILE:HD11	1.87	0.56
65:SB:202:GLN:O	82:S2:1121:G:N2	2.39	0.56
70:SI:70:GLU:OE2	72:SL:21:LYS:NZ	2.34	0.56
82:S2:207:G:H3'	82:S2:208:G:H8	1.69	0.56
82:S2:609:U:H2'	82:S2:610:G:H8	1.71	0.56
82:S2:677:G:N1	82:S2:1027:A:OP2	2.33	0.56
2:L5:4618:OMG:H5'	25:LV:15:ARG:HB2	1.86	0.56
68:SG:48:TYR:HE1	68:SG:117:GLY:H	1.52	0.56
70:SI:56:ARG:NH2	82:S2:380:G:OP1	2.39	0.56
74:SO:135:ILE:O	82:S2:943:U:O2'	2.23	0.56
2:L5:399:G:N2	19:LP:101:ASN:OD1	2.36	0.56
2:L5:4935:C:H2'	2:L5:4936:G:C8	2.41	0.56
49:SD:132:LYS:HD3	49:SD:189:MET:HE2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SG:132:ARG:NH2	82:S2:151:C:O2	2.33	0.56
69:SH:7:LYS:HD3	69:SH:10:LYS:HB3	1.88	0.56
48:Lt:12:VAL:HG11	48:Lt:65:GLN:H	1.70	0.56
54:SQ:97:GLN:HE22	63:Sg:58:ALA:HB3	1.70	0.56
65:SB:30:TRP:CH2	65:SB:48:LEU:HD23	2.41	0.56
2:L5:1523:A:N3	2:L5:4389:C:O2'	2.36	0.55
2:L5:2909:C:O2'	2:L5:3585:G:N1	2.37	0.55
2:L5:3777:G:O2'	2:L5:3815:G:O6	2.21	0.55
2:L5:4113:U:H4'	2:L5:4115:G:C6	2.40	0.55
6:LB:184:GLN:HE21	6:LB:186:ASN:HD21	1.54	0.55
10:LF:41:MET:HG3	31:Lb:109:ARG:HD2	1.87	0.55
13:LI:31:ILE:HG22	13:LI:62:SER:HB2	1.86	0.55
14:LJ:120:ASP:OD2	14:LJ:122:SER:OG	2.22	0.55
24:LU:99:TRP:HZ3	84:CI:58:LEU:CA	2.17	0.55
47:Ls:91:THR:OG1	47:Ls:93:GLU:OE1	2.24	0.55
58:SU:40:ILE:O	58:SU:44:LYS:HG2	2.06	0.55
77:SX:129:SER:HB3	82:S2:29:G:H4'	1.88	0.55
2:L5:3898:G:H5'	6:LB:254:ILE:HG13	1.88	0.55
24:LU:116:GLN:O	84:CI:74:LYS:CA	2.49	0.55
56:SS:46:ARG:NH2	57:ST:47:PRO:O	2.39	0.55
67:SE:131:VAL:HA	67:SE:137:PRO:HA	1.87	0.55
72:SL:49:GLU:HG3	72:SL:118:ARG:HH21	1.71	0.55
82:S2:1560:U:O2	82:S2:1575:G:O6	2.24	0.55
10:LF:50:ILE:HD12	10:LF:186:CYS:HB3	1.88	0.55
82:S2:1382:A:H2'	82:S2:1383:A2M:H8	1.88	0.55
1:Pt:50:U:O4	1:Pt:64:G:O6	2.25	0.55
2:L5:1464:C:H5''	31:Lb:32:LEU:HD12	1.88	0.55
2:L5:4537:C:H2'	2:L5:4538:G:H8	1.70	0.55
24:LU:99:TRP:CE3	84:CI:58:LEU:CD2	2.87	0.55
40:Lk:24:LYS:HD3	40:Lk:69:LEU:HD21	1.88	0.55
82:S2:51:U:H2'	82:S2:52:G:H8	1.72	0.55
82:S2:640:A:H2'	82:S2:641:A:C8	2.42	0.55
83:Zt:36:U:O2'	83:Zt:38:A:N7	2.39	0.55
2:L5:966:A:H5''	2:L5:2092:G:H22	1.71	0.55
2:L5:1187:G:H1'	8:LD:275:GLN:HE21	1.72	0.55
2:L5:1558:A:H2'	2:L5:1559:G:C8	2.41	0.55
2:L5:3798:U:OP2	25:LV:74:LYS:NZ	2.35	0.55
10:LF:213:LEU:HD13	10:LF:247:MET:HG2	1.88	0.55
67:SE:10:LYS:NZ	82:S2:95:G:OP1	2.30	0.55
67:SE:108:ARG:NH1	82:S2:847:A:OP1	2.40	0.55
2:L5:3736:A:H2'	2:L5:3737:A:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:141:C:H2'	4:L8:142:U:C6	2.42	0.55
17:LN:149:GLN:NE2	37:Lh:99:GLU:O	2.40	0.55
19:LP:35:ALA:HB2	19:LP:58:VAL:HG23	1.88	0.55
20:LQ:50:ARG:HH21	20:LQ:140:SER:HB2	1.72	0.55
49:SD:40:ARG:NH2	58:SU:106:ILE:O	2.38	0.55
62:Sf:105:TYR:HD2	62:Sf:118:ARG:HG3	1.71	0.55
63:Sg:131:LEU:O	63:Sg:139:LYS:N	2.36	0.55
78:SY:11:LYS:NZ	82:S2:832:G:O6	2.40	0.55
82:S2:902:G:O2'	82:S2:903:A:O4'	2.25	0.55
82:S2:1013:U:OP1	82:S2:1129:G:O2'	2.23	0.55
82:S2:1128:C:H2'	82:S2:1129:G:H8	1.71	0.55
2:L5:2411:C:H2'	2:L5:2412:A:C8	2.41	0.55
2:L5:4420:U:H5''	2:L5:4421:C:H5	1.71	0.55
2:L5:4967:A:H2'	2:L5:4968:A:H8	1.70	0.55
55:SR:114:LEU:HD23	55:SR:116:ASN:H	1.70	0.55
63:Sg:129:ILE:HB	63:Sg:142:VAL:HB	1.89	0.55
70:SI:54:LYS:NZ	82:S2:381:C:OP2	2.38	0.55
74:SO:34:PHE:HB3	74:SO:41:PHE:HB2	1.88	0.55
82:S2:496:C:H2'	82:S2:497:C:H6	1.71	0.55
82:S2:1115:U:O2'	82:S2:1117:C:OP2	2.24	0.55
82:S2:1291:A:OP2	82:S2:1302:G:O2'	2.20	0.55
2:L5:3917:A:H2'	2:L5:3918:G:H8	1.72	0.55
2:L5:4084:G:O6	5:LA:70:LYS:NZ	2.35	0.55
2:L5:4532:PSU:OP2	2:L5:4554:G:N1	2.30	0.55
60:Sc:29:GLN:HA	60:Sc:45:ASN:HA	1.89	0.55
68:SG:41:LEU:HG	68:SG:45:TRP:CD1	2.42	0.55
70:SI:45:THR:HG23	70:SI:53:LYS:HG3	1.87	0.55
1:Pt:47:U:O2'	1:Pt:50:U:OP1	2.24	0.55
2:L5:173:C:OP1	15:LL:129:ARG:NH1	2.40	0.55
33:Ld:90:ARG:HD3	33:Ld:102:LEU:HD13	1.88	0.55
53:SP:79:HIS:HD2	82:S2:1298:G:C4	2.25	0.55
68:SG:66:GLY:HA2	82:S2:1745:A:H1'	1.88	0.55
70:SI:84:ASN:HD22	70:SI:100:CYS:HB3	1.72	0.55
83:Zt:52:G:O2'	83:Zt:53:G:OP1	2.23	0.55
2:L5:1567:U:OP1	45:Lp:3:LYS:NZ	2.37	0.55
2:L5:4992:G:H2'	2:L5:4993:G:C8	2.42	0.55
6:LB:206:PRO:HG2	6:LB:209:GLN:HG3	1.88	0.55
50:SF:142:SER:HB3	60:Sc:50:VAL:HG22	1.88	0.55
54:SQ:31:LEU:HD12	54:SQ:33:LYS:HE2	1.89	0.55
66:SC:79:GLU:OE1	66:SC:79:GLU:N	2.40	0.55
66:SC:144:SER:HB3	66:SC:150:ALA:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3911:C:H2'	2:L5:3912:U:H6	1.71	0.54
47:Ls:110:ALA:HA	47:Ls:182:PRO:HG2	1.89	0.54
68:SG:191:ARG:HH22	82:S2:312:G:H2'	1.72	0.54
72:SL:93:LEU:HD21	77:SX:8:ARG:HD3	1.88	0.54
2:L5:173:C:H2'	2:L5:174:C:C6	2.42	0.54
2:L5:2848:G:O2'	2:L5:3838:U:O4	2.23	0.54
15:LL:170:THR:OG1	15:LL:173:GLU:OE1	2.18	0.54
43:Ln:1:MET:HG3	82:S2:1706:G:H5'	1.89	0.54
50:SF:60:ARG:HD2	82:S2:1679:A:H2'	1.89	0.54
82:S2:940:U:H3	82:S2:1002:U:H3	1.55	0.54
1:Pt:73:A:N3	13:LI:110:ARG:NH1	2.55	0.54
2:L5:303:C:OP2	17:LN:68:ARG:NH2	2.39	0.54
2:L5:2082:G:O2'	10:LF:164:LYS:NZ	2.35	0.54
21:LR:49:LEU:CD2	84:CI:75:LYS:HG3	2.37	0.54
40:Lk:17:ARG:NH2	40:Lk:19:ASP:OD2	2.39	0.54
46:Lr:90:LEU:HD22	46:Lr:111:ILE:HG23	1.89	0.54
47:Ls:13:TYR:O	47:Ls:17:ILE:HD12	2.06	0.54
53:SP:47:ARG:NH2	82:S2:1619:A:OP2	2.37	0.54
57:ST:96:SER:OG	82:S2:1568:C:OP1	2.24	0.54
68:SG:7:PHE:HB2	68:SG:113:ILE:HD12	1.88	0.54
2:L5:1701:A:H5'	7:LC:304:ALA:HB3	1.89	0.54
2:L5:4478:G:O2'	2:L5:4602:A:N1	2.38	0.54
2:L5:4893:A:OP1	18:LO:188:LYS:NZ	2.36	0.54
2:L5:4910:G:H4'	6:LB:95:THR:HG22	1.89	0.54
2:L5:4941:G:OP2	9:LE:188:ARG:NH2	2.27	0.54
2:L5:4991:U:H2'	2:L5:4992:G:C8	2.43	0.54
6:LB:35:ASP:OD2	6:LB:193:LYS:NZ	2.40	0.54
16:LM:38:VAL:HG21	16:LM:50:MET:HB3	1.90	0.54
24:LU:23:LEU:N	24:LU:70:ILE:O	2.32	0.54
51:SK:12:TYR:HB3	51:SK:79:LEU:HD11	1.88	0.54
71:SJ:18:ARG:HH22	82:S2:4:C:H1'	1.70	0.54
74:SO:61:LYS:NZ	74:SO:80:ASP:OD2	2.33	0.54
74:SO:149:ARG:NH2	82:S2:961:G:OP1	2.41	0.54
82:S2:604:A:N3	82:S2:639:C:O2'	2.34	0.54
2:L5:1703:C:O2'	2:L5:1704:C:O5'	2.24	0.54
2:L5:2101:C:H2'	2:L5:2102:G:C8	2.43	0.54
2:L5:2756:G:O6	29:LZ:51:ARG:NH2	2.30	0.54
2:L5:3880:G:H2'	2:L5:3881:G:C8	2.42	0.54
24:LU:28:PRO:HB2	24:LU:34:MET:HG3	1.89	0.54
24:LU:99:TRP:HE3	84:CI:58:LEU:HD23	1.70	0.54
55:SR:80:ARG:HE	64:SA:210:ILE:HG12	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1457:G:O2'	20:LQ:75:ARG:NH2	2.39	0.54
47:Ls:132:PRO:HB3	47:Ls:147:ILE:HD13	1.88	0.54
74:SO:40:THR:HG21	74:SO:74:ALA:HB2	1.89	0.54
82:S2:1217:A:H2'	82:S2:1218:C:C6	2.42	0.54
2:L5:1371:A:N1	4:L8:28:C:O2'	2.40	0.54
2:L5:2545:U:N3	4:L8:124:U:OP1	2.39	0.54
67:SE:247:THR:N	67:SE:250:GLU:OE2	2.39	0.54
82:S2:996:A:H2'	82:S2:997:A:C8	2.43	0.54
2:L5:1976:G:O6	2:L5:1990:A:N1	2.41	0.54
2:L5:2521:G:H4'	36:Lg:26:PRO:HD2	1.89	0.54
4:L8:8:U:H2'	4:L8:9:A:H8	1.71	0.54
8:LD:211:LEU:HB3	8:LD:219:TYR:HB2	1.90	0.54
28:LY:30:MET:HE1	28:LY:75:ARG:HA	1.90	0.54
63:Sg:18:VAL:O	63:Sg:287:THR:OG1	2.26	0.54
69:SH:138:GLU:OE1	73:SN:19:ARG:NE	2.41	0.54
83:Zt:69:G:H2'	83:Zt:70:G:H8	1.71	0.54
2:L5:387:G:HO2'	2:L5:412:G:H1	1.55	0.54
2:L5:662:C:N4	2:L5:663:G:O6	2.41	0.54
2:L5:1339:U:H2'	2:L5:1340:OMC:C6	2.42	0.54
2:L5:4523:A2M:H5''	2:L5:4524:G:H5'	1.90	0.54
14:LJ:95:ARG:HD2	14:LJ:177:GLY:HA3	1.89	0.54
26:LW:81:ALA:HB2	26:LW:87:LEU:HG	1.90	0.54
33:Ld:57:MET:HG2	33:Ld:88:LEU:HD23	1.90	0.54
44:Lo:78:ARG:O	44:Lo:80:LYS:NZ	2.40	0.54
53:SP:44:ARG:NH2	53:SP:47:ARG:O	2.41	0.54
54:SQ:78:VAL:HG22	82:S2:1673:U:H5''	1.90	0.54
78:SY:78:SER:OG	78:SY:80:ASP:OD1	2.25	0.54
82:S2:1284:A:N6	82:S2:1313:A:O2'	2.41	0.54
2:L5:327:U:O2'	38:Li:30:ARG:NH1	2.41	0.54
2:L5:935:A:O2'	16:LM:44:GLN:O	2.22	0.54
2:L5:2758:G:O2'	2:L5:2765:A:N3	2.31	0.54
2:L5:4097:G:O6	2:L5:4098:A:N6	2.41	0.54
2:L5:4212:A:N1	23:LT:3:ASN:ND2	2.51	0.54
5:LA:229:ALA:HB3	5:LA:234:LYS:HB3	1.90	0.54
6:LB:145:GLN:HA	6:LB:148:LYS:HD3	1.90	0.54
46:Lr:39:ARG:O	46:Lr:103:ARG:NH2	2.38	0.54
49:SD:33:GLY:HA3	49:SD:53:THR:HG22	1.90	0.54
54:SQ:25:CYS:HA	54:SQ:68:ILE:HG12	1.89	0.54
63:Sg:74:ASP:OD2	63:Sg:76:GLN:NE2	2.40	0.54
63:Sg:206:LEU:HD12	63:Sg:218:LEU:HD11	1.90	0.54
65:SB:39:PHE:HE1	65:SB:189:ILE:HD11	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Sb:14:GLU:HA	80:Sb:17:ARG:HG2	1.88	0.54
82:S2:1284:A:OP1	82:S2:1285:G:O2'	2.24	0.54
2:L5:2257:C:H2'	2:L5:2260:C:H41	1.73	0.53
2:L5:3726:A:H2'	2:L5:3727:A:C8	2.43	0.53
2:L5:4501:U:OP1	6:LB:5:LYS:NZ	2.40	0.53
4:L8:67:U:H2'	4:L8:68:G:H8	1.73	0.53
13:LI:101:LYS:NZ	13:LI:102:MET:O	2.37	0.53
51:SK:8:ARG:HH12	82:S2:1314:U:H4'	1.73	0.53
81:Se:37:GLN:O	81:Se:41:ARG:NH1	2.41	0.53
2:L5:513:U:O2'	2:L5:646:G:O6	2.25	0.53
2:L5:1899:G:O2'	34:Le:57:ASN:OD1	2.26	0.53
2:L5:2799:G:O2'	39:Lj:6:SER:OG	2.22	0.53
2:L5:4736:C:H2'	2:L5:4737:G:H8	1.74	0.53
6:LB:95:THR:OG1	6:LB:98:GLY:O	2.21	0.53
41:LI:9:ILE:HD11	41:LI:51:LEU:HD13	1.91	0.53
61:Sd:44:ARG:HH12	82:S2:1337:4AC:H5'	1.73	0.53
74:SO:45:THR:HA	74:SO:52:THR:HA	1.88	0.53
76:SW:106:THR:HG23	76:SW:108:ALA:H	1.73	0.53
78:SY:104:ARG:NH1	82:S2:507:G:OP2	2.38	0.53
2:L5:1637:A:OP1	2:L5:1640:C:N4	2.38	0.53
2:L5:2745:A:H2'	2:L5:2746:A:H8	1.73	0.53
2:L5:4107:G:N2	2:L5:4108:G:O6	2.40	0.53
2:L5:4260:U:H2'	2:L5:4261:C:C6	2.44	0.53
2:L5:4302:U:H4'	23:LT:5:LYS:HD3	1.90	0.53
2:L5:4967:A:H2'	2:L5:4968:A:C8	2.42	0.53
50:SF:20:PHE:HD2	50:SF:23:TRP:HZ3	1.57	0.53
53:SP:57:LEU:HB3	53:SP:61:ARG:NH1	2.23	0.53
68:SG:132:ARG:HD2	68:SG:133:LEU:HD22	1.91	0.53
69:SH:93:VAL:HG11	69:SH:133:LEU:HD12	1.89	0.53
74:SO:56:VAL:HG22	74:SO:81:VAL:HG23	1.90	0.53
82:S2:649:PSU:H2'	82:S2:650:A:H8	1.73	0.53
82:S2:1393:G:H2'	82:S2:1394:G:C8	2.43	0.53
83:Zt:9:A:H1'	83:Zt:45:G:H2'	1.90	0.53
83:Zt:49:C:H2'	83:Zt:50:A:H8	1.73	0.53
2:L5:4063:U:H2'	2:L5:4064:C:C6	2.43	0.53
9:LE:173:LEU:HD21	9:LE:191:GLN:HB3	1.90	0.53
49:SD:116:ARG:HD3	49:SD:152:PHE:HZ	1.74	0.53
54:SQ:80:GLN:O	54:SQ:84:ILE:HD12	2.09	0.53
82:S2:106:C:H2'	82:S2:107:A:H8	1.74	0.53
82:S2:835:C:H5'	82:S2:836:G:H5'	1.90	0.53
1:Pt:23:C:H2'	1:Pt:24:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2491:C:H2'	2:L5:2492:C:C6	2.43	0.53
10:LF:106:ARG:O	10:LF:110:GLN:HG3	2.08	0.53
14:LJ:43:LEU:HD13	14:LJ:117:ILE:HD11	1.91	0.53
18:LO:54:TYR:CD2	18:LO:145:VAL:HG21	2.43	0.53
54:SQ:51:LEU:HD22	54:SQ:81:ILE:HG23	1.91	0.53
63:Sg:21:ILE:HD11	63:Sg:307:VAL:HG21	1.91	0.53
82:S2:145:G:H2'	82:S2:146:G:H8	1.74	0.53
82:S2:325:C:N3	82:S2:326:C:O2'	2.39	0.53
2:L5:655:C:OP1	7:LC:268:ARG:NH2	2.42	0.53
17:LN:120:TRP:HZ2	17:LN:123:GLU:HG2	1.73	0.53
26:LW:123:LYS:HD2	82:S2:320:G:H5''	1.91	0.53
39:Lj:2:THR:O	39:Lj:7:SER:OG	2.21	0.53
47:Ls:31:GLY:HA2	47:Ls:86:VAL:HG12	1.89	0.53
48:Lt:114:ARG:HH21	48:Lt:119:ARG:HE	1.57	0.53
62:Sf:135:HIS:ND1	82:S2:1307:U:O2'	2.40	0.53
67:SE:18:TRP:HH2	67:SE:31:PRO:HD3	1.73	0.53
69:SH:69:LEU:HD12	69:SH:96:ALA:HB2	1.91	0.53
80:Sb:54:VAL:HG23	80:Sb:63:LEU:HB2	1.88	0.53
82:S2:808:A:H2	82:S2:855:G:H22	1.57	0.53
82:S2:942:G:H2'	82:S2:943:U:C6	2.44	0.53
82:S2:1304:U:H2'	82:S2:1305:C:C6	2.44	0.53
82:S2:1545:A:N3	82:S2:1671:G:O2'	2.32	0.53
2:L5:1328:G:O2'	2:L5:2349:A:OP1	2.26	0.53
2:L5:4966:A:H5''	6:LB:128:LYS:HG3	1.90	0.53
13:LI:31:ILE:HA	13:LI:66:GLU:OE2	2.08	0.53
53:SP:124:LYS:HD3	82:S2:1239:U:H5''	1.90	0.53
77:SX:54:LYS:HE3	77:SX:91:LEU:HG	1.91	0.53
82:S2:5:U:H2'	82:S2:6:G:H8	1.73	0.53
2:L5:4363:A:H5''	44:Lo:36:GLN:HG2	1.90	0.53
5:LA:101:VAL:HG22	5:LA:165:VAL:HG22	1.89	0.53
12:LH:173:ARG:NH1	42:Lm:125:LYS:O	2.36	0.53
14:LJ:65:ASN:HD21	44:Lo:101:GLY:HA2	1.73	0.53
16:LM:119:ARG:HG3	18:LO:189:ILE:HG23	1.89	0.53
58:SU:20:ILE:HG22	58:SU:116:ILE:HG22	1.90	0.53
69:SH:177:TYR:O	69:SH:181:THR:OG1	2.22	0.53
82:S2:1144:A:H2'	82:S2:1145:A:C8	2.43	0.53
2:L5:2111:G:N2	2:L5:2251:G:O2'	2.42	0.53
2:L5:4092:G:N7	2:L5:4114:C:N4	2.56	0.53
9:LE:164:PHE:HA	9:LE:175:VAL:HG12	1.89	0.53
56:SS:98:VAL:HG21	56:SS:103:LEU:HD13	1.89	0.53
67:SE:79:ASP:HB3	67:SE:82:TYR:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SJ:33:GLY:HA3	81:Se:38:TYR:CG	2.44	0.53
72:SL:74:SER:HA	72:SL:127:THR:HA	1.89	0.53
82:S2:525:A:H2'	82:S2:526:A:H8	1.72	0.53
82:S2:1598:G:N2	82:S2:1599:U:O4	2.41	0.53
82:S2:1683:C:H2'	82:S2:1684:C:H6	1.73	0.53
2:L5:2029:A:H2'	2:L5:2030:A:C8	2.43	0.53
2:L5:2706:G:N7	84:CI:78:HIS:NE2	2.57	0.53
2:L5:4088:C:H2'	2:L5:4089:G:H8	1.74	0.53
2:L5:4954:G:H2'	2:L5:4955:A:C8	2.44	0.53
6:LB:46:PHE:CE1	6:LB:84:MET:HG2	2.44	0.53
11:LG:162:ASP:HB3	11:LG:163:PRO:HD3	1.90	0.53
12:LH:92:MET:HG2	12:LH:181:VAL:HA	1.90	0.53
21:LR:99:MET:HE2	21:LR:99:MET:HA	1.91	0.53
24:LU:117:ILE:C	84:CI:75:LYS:O	2.52	0.53
34:Le:69:MET:HE3	34:Le:73:GLY:HA2	1.91	0.53
51:SK:29:MET:HE1	51:SK:33:PRO:HD3	1.91	0.53
52:SM:96:ARG:NH2	52:SM:100:PRO:O	2.41	0.53
2:L5:2443:G:OP2	2:L5:2516:G:N2	2.42	0.52
2:L5:4274:A:H2'	2:L5:4275:G:H8	1.73	0.52
2:L5:4775:C:H41	2:L5:4859:C:H42	1.58	0.52
12:LH:128:MET:HB3	12:LH:132:VAL:HG13	1.90	0.52
20:LQ:15:ARG:NH1	20:LQ:52:PHE:O	2.42	0.52
54:SQ:42:ILE:HG23	54:SQ:44:PRO:HD2	1.90	0.52
64:SA:159:ILE:HD11	75:SV:34:MET:HE1	1.92	0.52
2:L5:4575:G:O2'	2:L5:5069:U:OP1	2.27	0.52
6:LB:80:GLU:OE1	6:LB:323:TYR:OH	2.22	0.52
7:LC:334:THR:HG22	7:LC:337:ARG:HH21	1.74	0.52
10:LF:169:LEU:HB3	10:LF:187:MET:HE1	1.92	0.52
14:LJ:24:ILE:HG12	14:LJ:128:LEU:HB3	1.91	0.52
27:LX:82:THR:HA	27:LX:87:MET:HE3	1.91	0.52
49:SD:66:ILE:HD12	49:SD:69:LEU:HD11	1.91	0.52
54:SQ:15:ARG:HH22	82:S2:1444:U:P	2.32	0.52
64:SA:102:ARG:NH1	82:S2:1378:A:OP2	2.42	0.52
67:SE:29:PRO:HA	82:S2:496:C:H5'	1.91	0.52
2:L5:224:U:O2	7:LC:219:LYS:NZ	2.42	0.52
2:L5:1332:C:H2'	2:L5:1333:A:C8	2.43	0.52
2:L5:1962:A:H2	2:L5:2024:G:H21	1.56	0.52
2:L5:2261:G:H4'	9:LE:112:MET:HE3	1.92	0.52
2:L5:4537:C:H2'	2:L5:4538:G:C8	2.44	0.52
19:LP:47:TYR:O	19:LP:51:VAL:HG23	2.09	0.52
34:Le:12:ILE:HG12	34:Le:66:THR:HG23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lp:37:TYR:CD2	45:Lp:71:TYR:HB2	2.44	0.52
48:Lt:16:ARG:HH21	48:Lt:61:LYS:HG3	1.75	0.52
50:SF:51:HIS:NE2	82:S2:1674:G:OP1	2.40	0.52
61:Sd:7:TYR:OH	82:S2:1274:G:N7	2.32	0.52
77:SX:28:LYS:HE2	77:SX:32:LEU:HD22	1.91	0.52
82:S2:1203:G:H2'	82:S2:1204:A:H8	1.74	0.52
2:L5:32:G:OP1	17:LN:73:ARG:NH1	2.43	0.52
2:L5:1996:C:N4	2:L5:2000:G:H22	2.06	0.52
2:L5:2017:A:HO2'	2:L5:2018:C:P	2.32	0.52
2:L5:3954:A:H1'	2:L5:4058:U:H5'	1.92	0.52
2:L5:4882:U:OP1	16:LM:117:LYS:NZ	2.43	0.52
2:L5:4896:G:H2'	2:L5:4897:G:C8	2.45	0.52
2:L5:5046:U:P	33:Ld:83:ARG:HH12	2.32	0.52
5:LA:206:PRO:HG3	5:LA:213:GLY:HA3	1.91	0.52
52:SM:19:GLN:HE22	52:SM:88:TRP:CG	2.28	0.52
69:SH:105:THR:HG23	69:SH:107:LYS:H	1.74	0.52
2:L5:148:C:OP2	11:LG:197:LYS:NZ	2.39	0.52
2:L5:1680:G:O6	86:L5:5263:SPM:N1	2.43	0.52
7:LC:159:GLU:HA	7:LC:217:ILE:HB	1.91	0.52
8:LD:64:ILE:HD13	8:LD:109:LEU:HD22	1.90	0.52
10:LF:220:MET:HB3	10:LF:232:ASP:OD2	2.09	0.52
53:SP:44:ARG:HH11	82:S2:1619:A:H5'	1.74	0.52
57:ST:39:LEU:HD21	57:ST:52:TRP:CZ3	2.44	0.52
57:ST:101:ARG:NH1	82:S2:1566:G:O6	2.40	0.52
62:Sf:124:ASP:OD1	62:Sf:124:ASP:N	2.42	0.52
82:S2:1030:A:H2'	82:S2:1031:A2M:H8	1.90	0.52
2:L5:325:U:H2'	2:L5:326:C:C6	2.44	0.52
2:L5:1282:G:OP2	9:LE:128:HIS:NE2	2.42	0.52
2:L5:1538:U:H2'	2:L5:1539:G:H8	1.74	0.52
2:L5:4594:U:H2'	2:L5:4595:G:C8	2.45	0.52
3:L7:49:A:H5''	8:LD:224:SER:HB3	1.92	0.52
22:LS:15:ARG:HD2	22:LS:25:PRO:HG2	1.91	0.52
54:SQ:45:ARG:O	54:SQ:48:GLN:NE2	2.43	0.52
54:SQ:116:ASP:OD1	54:SQ:118:THR:OG1	2.20	0.52
78:SY:80:ASP:OD1	78:SY:81:TYR:N	2.42	0.52
82:S2:553:U:O4	82:S2:554:A:N6	2.38	0.52
2:L5:364:G:O6	39:Lj:55:ARG:NH2	2.42	0.52
2:L5:438:G:N2	35:Lf:23:GLU:OE2	2.43	0.52
2:L5:1333:A:H2'	2:L5:1334:A:C8	2.45	0.52
2:L5:4260:U:H2'	2:L5:4261:C:H6	1.75	0.52
2:L5:4694:G:H4'	12:LH:71:ARG:HH12	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:5027:C:OP2	70:SI:77:ARG:NH2	2.42	0.52
9:LE:264:ILE:HD11	9:LE:267:LEU:HD22	1.91	0.52
10:LF:38:ALA:HA	10:LF:41:MET:HE2	1.92	0.52
13:LI:207:ASP:HA	13:LI:210:ARG:HG2	1.92	0.52
48:Lt:105:THR:HG22	48:Lt:107:ASP:HB2	1.92	0.52
50:SF:168:THR:OG1	50:SF:171:GLU:OE1	2.27	0.52
64:SA:80:ARG:HH21	64:SA:126:ASP:HB2	1.74	0.52
72:SL:23:VAL:HG23	72:SL:25:LEU:HG	1.92	0.52
82:S2:107:A:H61	82:S2:354:OMU:HN3	1.57	0.52
82:S2:857:U:H2'	82:S2:858:A:C8	2.43	0.52
82:S2:885:U:O2	82:S2:901:G:O6	2.28	0.52
1:Pt:18:G:H21	1:Pt:58:A:H5'	1.75	0.52
2:L5:667:A:N3	46:Lr:46:ARG:NH1	2.58	0.52
2:L5:1403:G:N7	2:L5:1408:G:N2	2.57	0.52
2:L5:2643:G:H1'	40:Lk:3:ARG:NH2	2.25	0.52
7:LC:162:LYS:N	7:LC:166:GLU:OE2	2.37	0.52
20:LQ:151:HIS:ND1	20:LQ:164:LYS:O	2.41	0.52
39:Lj:27:TYR:HA	39:Lj:34:CYS:HA	1.92	0.52
51:SK:49:MET:HG2	51:SK:52:LEU:HD12	1.92	0.52
69:SH:83:LEU:HB3	69:SH:92:VAL:HG21	1.91	0.52
71:SJ:162:ARG:NH1	82:S2:582:U:OP1	2.43	0.52
77:SX:132:ALA:O	77:SX:136:GLY:N	2.43	0.52
82:S2:1139:C:H2'	82:S2:1140:G:O4'	2.10	0.52
82:S2:1568:C:H2'	82:S2:1569:A:C8	2.45	0.52
83:Zt:43:A:H3'	83:Zt:44:G:H8	1.74	0.52
2:L5:85:G:O2'	2:L5:97:G:O6	2.27	0.52
2:L5:1326:A2M:OP2	2:L5:4445:U:O2'	2.25	0.52
2:L5:1912:G:N2	18:LO:87:MET:HE2	2.25	0.52
2:L5:4225:G:OP1	13:LI:24:ARG:NH2	2.43	0.52
8:LD:52:ILE:HA	8:LD:147:ASP:HB3	1.91	0.52
28:LY:47:MET:HE3	28:LY:115:ARG:HH21	1.74	0.52
82:S2:162:C:H2'	82:S2:163:U:O4'	2.10	0.52
2:L5:2000:G:O2'	2:L5:2001:G:N7	2.42	0.52
2:L5:2045:G:O6	2:L5:3870:C:O2'	2.28	0.52
2:L5:4139:G:H21	2:L5:4140:C:H41	1.57	0.52
2:L5:4708:A:N3	2:L5:4709:U:H5'	2.24	0.52
10:LF:53:LYS:NZ	10:LF:189:ASP:OD2	2.35	0.52
13:LI:36:LEU:HB2	13:LI:87:MET:HE2	1.91	0.52
66:SC:102:LEU:HD11	66:SC:130:ILE:HD12	1.91	0.52
69:SH:164:ASN:OD1	69:SH:165:ASN:ND2	2.43	0.52
82:S2:1101:U:H2'	82:S2:1102:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Pt:23:C:H2'	1:Pt:24:A:H8	1.75	0.51
2:L5:1933:G:H2'	2:L5:1934:A:C8	2.45	0.51
2:L5:2634:C:H2'	2:L5:2635:U:H6	1.75	0.51
6:LB:17:LEU:O	6:LB:19:ARG:N	2.43	0.51
24:LU:45:GLU:HA	24:LU:54:GLY:HA2	1.92	0.51
63:Sg:245:ARG:HB3	63:Sg:247:TRP:HE3	1.75	0.51
71:SJ:145:PRO:HD2	82:S2:522:A:H5''	1.91	0.51
82:S2:414:A:H2'	82:S2:415:A:H8	1.74	0.51
82:S2:429:C:H2'	82:S2:430:C:H6	1.74	0.51
2:L5:454:U:H2'	2:L5:455:C:O4'	2.10	0.51
2:L5:1982:G:H1'	2:L5:2010:A:H4'	1.93	0.51
2:L5:2094:G:O2'	2:L5:2095:A:N3	2.40	0.51
2:L5:4088:C:H2'	2:L5:4089:G:C8	2.45	0.51
23:LT:114:GLN:NE2	23:LT:118:GLU:OE1	2.43	0.51
54:SQ:90:LYS:HG2	54:SQ:120:LEU:HD13	1.92	0.51
58:SU:27:ARG:NH2	61:Sd:51:GLY:O	2.44	0.51
67:SE:61:VAL:HA	67:SE:64:ILE:HG12	1.92	0.51
68:SG:174:PRO:HB3	82:S2:65:C:C6	2.46	0.51
82:S2:511:U:H2'	82:S2:512:A:H8	1.75	0.51
82:S2:639:C:H2'	82:S2:640:A:C8	2.45	0.51
2:L5:382:G:N1	2:L5:385:A:OP2	2.41	0.51
2:L5:3619:G:H22	2:L5:3624:A:H1'	1.73	0.51
24:LU:24:ASP:HB3	24:LU:111:GLU:HB3	1.91	0.51
25:LV:21:PRO:HA	25:LV:54:ALA:HA	1.90	0.51
54:SQ:9:SER:OG	54:SQ:25:CYS:O	2.26	0.51
64:SA:184:ARG:HE	64:SA:191:ARG:HA	1.75	0.51
66:SC:167:ARG:HB3	66:SC:177:PRO:HB2	1.92	0.51
82:S2:463:C:O2'	82:S2:466:G:O6	2.26	0.51
82:S2:955:A:N1	82:S2:968:U:O2'	2.40	0.51
2:L5:1995:G:O2'	48:Lt:122:ALA:O	2.18	0.51
2:L5:4897:G:H2'	2:L5:4898:G:H8	1.76	0.51
8:LD:197:LYS:HB3	8:LD:202:GLN:HB2	1.92	0.51
14:LJ:39:VAL:HG21	14:LJ:126:TYR:HD2	1.76	0.51
18:LO:186:GLU:OE1	18:LO:186:GLU:N	2.43	0.51
49:SD:53:THR:HG23	49:SD:54:ARG:HG3	1.92	0.51
51:SK:16:PHE:HB2	51:SK:79:LEU:HD21	1.93	0.51
59:SZ:85:ARG:NH2	82:S2:1597:C:OP2	2.35	0.51
60:Sc:21:THR:OG1	60:Sc:22:GLY:N	2.43	0.51
63:Sg:150:TRP:HB2	63:Sg:170:TRP:CE3	2.45	0.51
64:SA:32:PHE:CD1	82:S2:1097:G:H4'	2.45	0.51
82:S2:835:C:H4'	82:S2:836:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1533:A:H2	82:S2:1536:G:N3	2.09	0.51
2:L5:411:G:H5''	2:L5:414:C:H1'	1.91	0.51
2:L5:691:C:H2'	2:L5:692:A:C8	2.46	0.51
2:L5:1283:G:N1	2:L5:2076:G:OP1	2.31	0.51
2:L5:1326:A2M:H2'	2:L5:1327:C:H6	1.75	0.51
2:L5:1426:G:N1	2:L5:1458:C:OP2	2.39	0.51
2:L5:1500:A:H5''	2:L5:1501:C:H5''	1.93	0.51
2:L5:1552:G:O2'	2:L5:1574:G:N2	2.33	0.51
2:L5:1645:C:H2'	2:L5:1646:A:C8	2.45	0.51
2:L5:1975:G:N2	2:L5:1983:A:OP1	2.39	0.51
2:L5:2411:C:H2'	2:L5:2412:A:H8	1.75	0.51
7:LC:10:VAL:O	7:LC:18:SER:OG	2.27	0.51
8:LD:138:GLN:HB2	8:LD:139:PRO:HD2	1.92	0.51
2:L5:1317:U:H2'	2:L5:1318:C:C6	2.46	0.51
2:L5:2763:U:H4'	2:L5:2764:A:H5''	1.91	0.51
59:SZ:66:LYS:HD3	59:SZ:111:ARG:HH12	1.75	0.51
65:SB:34:LYS:O	65:SB:98:THR:OG1	2.25	0.51
67:SE:204:SER:OG	67:SE:205:PHE:N	2.42	0.51
82:S2:140:C:H42	82:S2:313:A:H61	1.59	0.51
2:L5:515:C:H41	2:L5:647:G:H21	1.59	0.51
2:L5:717:U:H2'	2:L5:718:C:C6	2.45	0.51
2:L5:2489:C:H4'	2:L5:2491:C:H42	1.75	0.51
2:L5:2521:G:H5'	2:L5:2640:G:H1'	1.91	0.51
2:L5:3908:A:N7	2:L5:4449:A:N6	2.59	0.51
2:L5:4353:PSU:H5'	2:L5:4354:U:H5'	1.92	0.51
12:LH:48:LEU:HB2	12:LH:54:ARG:HB2	1.92	0.51
27:LX:149:VAL:O	27:LX:153:ILE:HG12	2.10	0.51
32:Lc:21:VAL:HG23	32:Lc:99:PRO:HA	1.93	0.51
39:Lj:25:LYS:HE3	41:Ll:51:LEU:HA	1.91	0.51
73:SN:55:ARG:HD3	82:S2:1017:U:H5'	1.93	0.51
82:S2:525:A:H2'	82:S2:526:A:C8	2.45	0.51
82:S2:1259:A:N6	82:S2:1519:U:O5'	2.43	0.51
2:L5:1725:U:H2'	2:L5:1726:U:H6	1.76	0.51
2:L5:1846:G:H2'	2:L5:1847:C:C6	2.46	0.51
2:L5:1972:G:C6	2:L5:1973:G:C6	2.99	0.51
2:L5:2533:C:OP1	27:LX:139:ARG:NH1	2.44	0.51
2:L5:4627:U:H4'	6:LB:373:LYS:HE2	1.92	0.51
2:L5:5057:C:H2'	2:L5:5058:A:C8	2.45	0.51
11:LG:209:SER:HA	11:LG:212:LYS:HG3	1.91	0.51
34:Le:85:LEU:HD21	34:Le:115:ALA:HB2	1.92	0.51
67:SE:38:LEU:HA	67:SE:41:CYS:SG	2.51	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:24:C:HO2'	82:S2:25:A:H8	1.59	0.51
82:S2:51:U:H2'	82:S2:52:G:C8	2.46	0.51
82:S2:563:G:O2'	82:S2:564:A:OP1	2.29	0.51
82:S2:878:G:H22	82:S2:908:A:H2	1.59	0.51
82:S2:1144:A:H5'	82:S2:1355:C:H41	1.76	0.51
82:S2:1695:A:N1	82:S2:1832:6MZ:O2'	2.42	0.51
2:L5:197:A:N3	2:L5:222:C:O2'	2.43	0.51
2:L5:318:A:H2'	2:L5:319:A:C8	2.46	0.51
2:L5:1172:C:O2'	2:L5:1173:G:H8	1.94	0.51
2:L5:1281:G:OP1	7:LC:316:LYS:NZ	2.36	0.51
5:LA:131:GLY:H	5:LA:169:VAL:HG13	1.76	0.51
29:LZ:10:VAL:O	29:LZ:83:THR:OG1	2.28	0.51
56:SS:24:ARG:HH21	56:SS:28:PHE:HB3	1.76	0.51
56:SS:145:THR:OG1	82:S2:1523:C:OP1	2.27	0.51
64:SA:76:VAL:HG12	64:SA:123:VAL:HB	1.91	0.51
67:SE:45:ILE:HG13	67:SE:61:VAL:HG11	1.93	0.51
72:SL:73:LEU:HD11	72:SL:109:MET:HE1	1.93	0.51
82:S2:1854:U:H2'	82:S2:1855:G:H8	1.76	0.51
1:Pt:3:C:H42	1:Pt:70:A:H61	1.59	0.51
2:L5:710:G:H2'	2:L5:711:A:H8	1.75	0.51
2:L5:733:A:OP1	22:LS:70:LYS:NZ	2.40	0.51
2:L5:1700:G:H5'	2:L5:1702:C:OP2	2.11	0.51
2:L5:1972:G:C6	2:L5:1973:G:O6	2.64	0.51
2:L5:2708:U:H1'	84:CI:79:ARG:HH22	1.77	0.51
2:L5:4139:G:O6	2:L5:4141:G:N2	2.43	0.51
2:L5:4740:G:O6	2:L5:4959:U:O2	2.28	0.51
58:SU:23:THR:HG23	58:SU:113:GLU:HB3	1.93	0.51
67:SE:72:ILE:HD12	67:SE:77:ARG:HB2	1.92	0.51
82:S2:106:C:OP1	82:S2:431:G:O2'	2.28	0.51
82:S2:1199:A:H2'	82:S2:1200:A:C8	2.45	0.51
83:Zt:34:U:H2'	83:Zt:35:U:C6	2.44	0.51
2:L5:1252:C:N4	2:L5:1253:G:N3	2.60	0.50
2:L5:1398:A:N1	2:L5:1419:G:O2'	2.44	0.50
2:L5:1869:G:C6	87:L5:5286:SPD:H32	2.46	0.50
2:L5:5064:G:N2	19:LP:75:GLN:HE22	2.05	0.50
32:Lc:80:GLU:HA	32:Lc:83:THR:HB	1.93	0.50
44:Lo:101:GLY:O	44:Lo:102:GLN:NE2	2.40	0.50
65:SB:87:ILE:H	65:SB:101:HIS:HB2	1.75	0.50
67:SE:121:TYR:HB2	67:SE:161:GLN:NE2	2.24	0.50
68:SG:227:GLN:HG3	68:SG:231:ARG:HH21	1.76	0.50
2:L5:439:G:H1'	35:Lf:23:GLU:OE1	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1461:C:H2'	2:L5:1462:A:C8	2.46	0.50
2:L5:2580:U:OP1	29:LZ:36:ARG:NH1	2.37	0.50
14:LJ:104:ASN:HD22	14:LJ:133:VAL:HG13	1.76	0.50
33:Ld:23:ARG:HG2	33:Ld:121:ASN:HA	1.92	0.50
48:Lt:79:ALA:HA	48:Lt:82:ILE:HG12	1.92	0.50
51:SK:31:LYS:NZ	51:SK:32:HIS:O	2.44	0.50
63:Sg:62:HIS:NE2	63:Sg:80:SER:OG	2.35	0.50
64:SA:137:ALA:HB1	64:SA:142:LEU:HB3	1.93	0.50
66:SC:147:VAL:O	66:SC:151:ILE:HD12	2.11	0.50
67:SE:179:ASN:HA	67:SE:231:GLY:HA2	1.93	0.50
82:S2:454:U:H2'	82:S2:455:A:H8	1.75	0.50
82:S2:659:G:O2'	82:S2:662:G:O2'	2.29	0.50
82:S2:1589:A:N3	82:S2:1653:U:O2'	2.42	0.50
83:Zt:49:C:H2'	83:Zt:50:A:C8	2.47	0.50
2:L5:679:C:H2'	2:L5:680:G:C8	2.45	0.50
2:L5:2459:G:N2	2:L5:2462:C:OP2	2.39	0.50
2:L5:3732:A:H2'	2:L5:3733:A:C8	2.46	0.50
3:L7:119:U:C2	8:LD:261:VAL:HG11	2.46	0.50
13:LI:28:ASP:HB3	13:LI:32:ARG:HH22	1.75	0.50
30:La:113:GLY:O	30:La:136:LYS:NZ	2.38	0.50
47:Ls:17:ILE:HG13	47:Ls:54:LEU:HD21	1.93	0.50
51:SK:31:LYS:HE2	51:SK:40:VAL:H	1.76	0.50
63:Sg:4:GLN:H	63:Sg:313:THR:HB	1.76	0.50
63:Sg:201:SER:OG	63:Sg:203:ASP:OD1	2.26	0.50
66:SC:263:LYS:HE3	66:SC:267:GLN:HG3	1.93	0.50
67:SE:139:LEU:HD22	67:SE:147:ILE:HD11	1.93	0.50
69:SH:144:ILE:HG23	69:SH:154:ILE:HG13	1.93	0.50
71:SJ:114:VAL:HG23	71:SJ:126:ALA:HB1	1.94	0.50
76:SW:11:LEU:HD12	76:SW:74:VAL:HB	1.94	0.50
82:S2:66:G:H2'	82:S2:67:C:H4'	1.93	0.50
82:S2:588:G:H4'	82:S2:589:G:H5'	1.93	0.50
82:S2:683:OMG:N1	82:S2:1022:U:OP2	2.37	0.50
82:S2:980:A:H2'	82:S2:981:A:C8	2.47	0.50
2:L5:460:C:H2'	2:L5:461:G:C8	2.46	0.50
2:L5:1548:G:O2'	2:L5:2812:A:N3	2.39	0.50
2:L5:1992:U:H4'	2:L5:1993:C:H5''	1.92	0.50
2:L5:4279:A:H5'	2:L5:4281:A:H1'	1.93	0.50
47:Ls:78:LEU:HD12	47:Ls:82:ILE:HD11	1.92	0.50
63:Sg:3:GLU:O	63:Sg:4:GLN:NE2	2.45	0.50
63:Sg:230:LEU:HD11	63:Sg:259:TRP:CD1	2.46	0.50
65:SB:140:VAL:HG13	65:SB:213:ARG:HD2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SH:46:THR:HG23	69:SH:65:PRO:HD3	1.93	0.50
70:SI:141:ARG:HD3	70:SI:145:ILE:HG21	1.92	0.50
78:SY:12:PHE:HZ	78:SY:21:LYS:HD2	1.77	0.50
82:S2:1337:4AC:O5'	82:S2:1337:4AC:H6	2.12	0.50
82:S2:1405:A:H2'	82:S2:1406:G:O4'	2.12	0.50
82:S2:1588:A:H2'	82:S2:1589:A:C8	2.46	0.50
82:S2:1658:G:OP2	82:S2:1660:C:N4	2.45	0.50
2:L5:2023:C:OP2	47:Ls:83:ARG:NH2	2.44	0.50
2:L5:2745:A:H2'	2:L5:2746:A:C8	2.47	0.50
2:L5:4077:A:N1	2:L5:4171:C:N4	2.60	0.50
4:L8:96:C:H5''	37:Lh:66:LYS:HG2	1.92	0.50
17:LN:68:ARG:NH1	17:LN:124:ASP:O	2.41	0.50
26:LW:80:ARG:NH1	82:S2:167:G:O2'	2.44	0.50
41:Ll:27:ILE:O	41:Ll:33:ASN:ND2	2.44	0.50
49:SD:160:SER:OG	82:S2:1386:A:OP2	2.24	0.50
65:SB:123:ALA:HB2	65:SB:165:ARG:HG2	1.94	0.50
68:SG:185:LEU:HB3	68:SG:189:ARG:NH1	2.27	0.50
79:Sa:6:ARG:NH1	82:S2:1147:C:OP1	2.39	0.50
82:S2:692:G:N7	82:S2:693:A:N6	2.59	0.50
82:S2:1419:C:H41	82:S2:1421:A:H2	1.60	0.50
2:L5:1414:C:H2'	2:L5:1415:G:C8	2.44	0.50
2:L5:4069:U:H2'	2:L5:4070:U:H6	1.76	0.50
2:L5:4769:G:H5''	18:LO:176:ARG:HD3	1.92	0.50
54:SQ:47:LEU:HD23	54:SQ:50:LYS:HG3	1.94	0.50
60:Sc:39:SER:HB2	79:Sa:51:ARG:HH12	1.76	0.50
76:SW:30:CYS:SG	76:SW:31:SER:N	2.84	0.50
2:L5:163:A:H2'	2:L5:164:G:H8	1.77	0.50
2:L5:1415:G:H2'	2:L5:1416:G:H8	1.77	0.50
2:L5:2483:G:H1	2:L5:2495:U:H3	1.58	0.50
20:LQ:97:LYS:NZ	20:LQ:117:GLY:O	2.41	0.50
25:LV:123:LYS:N	25:LV:140:ALA:OXT	2.45	0.50
47:Ls:109:ALA:O	47:Ls:184:SER:OG	2.24	0.50
56:SS:14:ARG:HH11	56:SS:19:ASN:HB3	1.77	0.50
65:SB:144:LYS:HB2	65:SB:208:HIS:HB3	1.94	0.50
82:S2:672:A:N6	82:S2:1027:A:OP1	2.40	0.50
82:S2:929:G:H2'	82:S2:930:C:O4'	2.11	0.50
2:L5:1628:C:OP1	5:LA:14:SER:OG	2.28	0.50
2:L5:2667:C:O4'	21:LR:96:MET:HG2	2.11	0.50
2:L5:4601:U:H2'	2:L5:4602:A:H8	1.76	0.50
22:LS:95:ARG:NH2	22:LS:112:ASP:OD2	2.44	0.50
28:LY:86:GLN:HG3	28:LY:94:THR:HB	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:SD:225:GLU:O	63:Sg:186:THR:OG1	2.19	0.50
50:SF:123:GLU:HG3	50:SF:140:ASP:HB3	1.94	0.50
63:Sg:120:ILE:HB	63:Sg:132:TRP:HB2	1.93	0.50
67:SE:212:ASP:OD1	67:SE:216:ASN:N	2.45	0.50
72:SL:133:PRO:HG2	82:S2:383:G:H21	1.77	0.50
74:SO:56:VAL:HG23	74:SO:77:ALA:HB1	1.93	0.50
2:L5:153:G:H2'	2:L5:154:G:H8	1.77	0.50
2:L5:1088:C:O2	10:LF:74:MET:HE1	2.12	0.50
2:L5:1291:G:OP1	9:LE:219:LYS:NZ	2.40	0.50
2:L5:1308:C:H2'	2:L5:1309:C:C6	2.46	0.50
2:L5:1390:G:N2	2:L5:1393:G:OP2	2.36	0.50
2:L5:1577:G:O2'	2:L5:1612:G:H4'	2.12	0.50
2:L5:1996:C:O2'	47:Ls:44:ARG:NE	2.44	0.50
2:L5:2021:G:OP1	47:Ls:58:ASN:N	2.39	0.50
2:L5:2808:G:O3'	21:LR:60:ARG:NH1	2.44	0.50
4:L8:62:A:OP1	37:Lh:52:LYS:NZ	2.39	0.50
23:LT:48:VAL:HG21	23:LT:94:GLU:HG2	1.92	0.50
49:SD:45:ARG:NH1	49:SD:47:GLU:OE1	2.45	0.50
51:SK:27:VAL:HG13	51:SK:28:HIS:CD2	2.47	0.50
51:SK:65:ARG:NH1	61:Sd:20:SER:OG	2.45	0.50
55:SR:44:LYS:HG3	55:SR:47:ARG:HH21	1.76	0.50
78:SY:77:ASP:OD1	78:SY:77:ASP:N	2.45	0.50
82:S2:747:U:N3	82:S2:796:G:N1	2.60	0.50
82:S2:1605:G:N2	82:S2:1633:A:OP2	2.41	0.50
1:Pt:26:G:O6	1:Pt:44:A:N1	2.45	0.49
2:L5:734:G:H22	2:L5:929:A:H2	1.59	0.49
2:L5:3664:G:H2'	2:L5:3665:G:H8	1.77	0.49
2:L5:4070:U:H2'	2:L5:4071:U:C6	2.47	0.49
2:L5:4522:G:O2'	2:L5:4525:C:OP2	2.22	0.49
5:LA:180:LEU:HD21	45:Lp:22:LEU:HB3	1.95	0.49
53:SP:28:MET:HG2	53:SP:33:LEU:HD13	1.94	0.49
55:SR:6:THR:HA	82:S2:1373:C:H5'	1.94	0.49
68:SG:2:LYS:HB3	68:SG:15:LEU:HD11	1.94	0.49
79:Sa:44:ILE:HG23	79:Sa:45:VAL:HG13	1.93	0.49
82:S2:528:A:H2'	82:S2:529:A:C8	2.46	0.49
82:S2:817:G:N2	82:S2:818:A:N7	2.60	0.49
82:S2:1347:U:H2'	82:S2:1348:G:N3	2.27	0.49
2:L5:2059:C:O2	22:LS:118:ARG:NH2	2.45	0.49
2:L5:2835:A:O2'	6:LB:228:TYR:O	2.23	0.49
2:L5:4991:U:H2'	2:L5:4992:G:H8	1.77	0.49
32:Lc:82:GLY:HA2	32:Lc:91:VAL:HG12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lg:44:SER:OG	36:Lg:46:CYS:SG	2.57	0.49
50:SF:42:LYS:HG3	50:SF:43:GLU:H	1.77	0.49
68:SG:51:ARG:N	68:SG:112:VAL:O	2.37	0.49
70:SI:65:PHE:CE2	70:SI:104:ILE:HG21	2.47	0.49
82:S2:496:C:H2'	82:S2:497:C:C6	2.47	0.49
82:S2:1206:G:O2'	82:S2:1208:A:OP1	2.23	0.49
2:L5:433:A:C2	2:L5:3867:A2M:H4'	2.47	0.49
2:L5:1281:G:N1	9:LE:128:HIS:HB2	2.26	0.49
2:L5:2764:A:H2'	2:L5:2765:A:H8	1.77	0.49
2:L5:3707:U:H2'	2:L5:3708:C:C6	2.47	0.49
2:L5:4699:U:H1'	2:L5:4700:A:H5''	1.94	0.49
5:LA:181:LYS:HB2	5:LA:184:ARG:HG3	1.95	0.49
17:LN:136:ASP:OD2	17:LN:139:HIS:N	2.46	0.49
52:SM:79:VAL:HG11	52:SM:85:LEU:HD22	1.94	0.49
58:SU:51:LYS:NZ	82:S2:1402:A:H4'	2.27	0.49
66:SC:94:ILE:HD11	66:SC:159:LYS:HG2	1.93	0.49
70:SI:166:PHE:HE1	70:SI:171:LEU:HD11	1.76	0.49
74:SO:149:ARG:NH1	82:S2:1064:C:O3'	2.44	0.49
82:S2:90:G:OP1	82:S2:445:A:N6	2.45	0.49
83:Zt:26:A:N1	83:Zt:44:G:N2	2.54	0.49
10:LF:83:VAL:HG12	22:LS:62:VAL:HA	1.94	0.49
20:LQ:122:THR:OG1	20:LQ:124:ASP:OD1	2.30	0.49
67:SE:88:ASP:OD1	67:SE:122:LYS:NZ	2.28	0.49
67:SE:100:ARG:HB2	67:SE:114:ILE:HD13	1.94	0.49
82:S2:5:U:H2'	82:S2:6:G:C8	2.48	0.49
82:S2:550:C:H2'	82:S2:551:U:C6	2.47	0.49
2:L5:1305:C:OP1	4:L8:7:U:O2'	2.31	0.49
2:L5:3696:C:O2'	2:L5:3816:A:N1	2.43	0.49
2:L5:3886:G:OP1	18:LO:85:ARG:NH2	2.44	0.49
7:LC:293:LEU:O	7:LC:299:GLN:NE2	2.46	0.49
11:LG:55:VAL:HG21	27:LX:41:ARG:HD2	1.93	0.49
14:LJ:144:LYS:HE2	14:LJ:146:ARG:O	2.11	0.49
29:LZ:22:LYS:NZ	29:LZ:132:GLN:O	2.39	0.49
47:Ls:62:ARG:HB3	47:Ls:66:ARG:NH1	2.28	0.49
54:SQ:15:ARG:NH1	54:SQ:20:THR:OG1	2.45	0.49
54:SQ:30:GLY:HA3	54:SQ:64:ALA:HA	1.93	0.49
61:Sd:12:ARG:O	82:S2:1556:A:N6	2.46	0.49
66:SC:60:TRP:CZ2	66:SC:62:PRO:HB3	2.48	0.49
67:SE:35:PRO:HB3	67:SE:143:ASP:HB3	1.93	0.49
82:S2:1208:A:H2'	82:S2:1209:A:H8	1.77	0.49
82:S2:1422:G:H4'	82:S2:1423:C:H3'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1512:C:H2'	82:S2:1513:C:C6	2.48	0.49
2:L5:109:G:OP2	15:LL:74:ARG:NH2	2.45	0.49
2:L5:519:C:H1'	2:L5:643:C:C2	2.48	0.49
2:L5:1895:G:OP1	10:LF:96:ARG:NH2	2.43	0.49
2:L5:2103:G:N7	2:L5:2104:G:N2	2.60	0.49
2:L5:2693:G:OP1	40:Lk:35:LYS:HE2	2.13	0.49
2:L5:3722:G:H2'	2:L5:3723:A:H8	1.77	0.49
11:LG:148:GLU:OE2	17:LN:6:TYR:OH	2.27	0.49
24:LU:99:TRP:CH2	84:CI:58:LEU:HB3	2.43	0.49
49:SD:99:ILE:HG23	49:SD:173:ARG:HH21	1.76	0.49
52:SM:58:GLU:HB3	52:SM:61:TYR:HB2	1.94	0.49
56:SS:14:ARG:NH2	56:SS:17:ASN:O	2.45	0.49
58:SU:27:ARG:NE	58:SU:82:MET:SD	2.72	0.49
74:SO:26:ASN:HB2	74:SO:91:THR:HG23	1.93	0.49
78:SY:41:ARG:NH2	78:SY:52:PRO:O	2.46	0.49
80:Sb:2:PRO:HB3	80:Sb:5:LYS:HE3	1.94	0.49
82:S2:931:C:H2'	82:S2:932:G:C8	2.46	0.49
2:L5:223:G:OP2	7:LC:165:LYS:NZ	2.45	0.49
2:L5:253:G:H2'	2:L5:254:G:C8	2.48	0.49
2:L5:737:C:C5	2:L5:739:G:H5''	2.48	0.49
2:L5:2744:A:H2'	2:L5:2745:A:C8	2.47	0.49
2:L5:3822:PSU:OP1	86:L5:5292:SPM:N5	2.46	0.49
2:L5:3932:U:H2'	2:L5:3933:G:H8	1.77	0.49
2:L5:4076:G:H5'	11:LG:73:ARG:HG3	1.94	0.49
2:L5:4476:C:O2'	2:L5:4478:G:OP2	2.25	0.49
4:L8:102:G:OP2	4:L8:104:A:O2'	2.26	0.49
6:LB:107:ALA:HB2	6:LB:201:LEU:HD22	1.93	0.49
27:LX:81:LEU:HG	27:LX:83:THR:HG23	1.95	0.49
51:SK:3:MET:HB2	51:SK:7:ASN:HD21	1.77	0.49
56:SS:55:ARG:N	56:SS:58:GLU:OE2	2.46	0.49
63:Sg:237:ASN:ND2	63:Sg:286:CYS:O	2.45	0.49
68:SG:67:VAL:HB	68:SG:99:GLY:HA2	1.94	0.49
69:SH:91:HIS:ND1	69:SH:169:LYS:HG2	2.28	0.49
70:SI:6:ASP:OD1	70:SI:9:HIS:ND1	2.45	0.49
76:SW:10:ALA:O	76:SW:14:ILE:HD12	2.12	0.49
82:S2:186:C:H2'	82:S2:187:G:H8	1.78	0.49
82:S2:520:A:O2'	82:S2:825:A:N3	2.41	0.49
82:S2:1189:A:H2'	82:S2:1190:A:H8	1.78	0.49
82:S2:1720:U:H5''	82:S2:1721:U:H5''	1.94	0.49
2:L5:457:G:H2'	2:L5:458:C:C6	2.47	0.49
2:L5:1097:C:H2'	2:L5:1098:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L8:57:C:OP2	39:Lj:68:LYS:NZ	2.46	0.49
8:LD:217:ASP:OD1	8:LD:218:ALA:N	2.46	0.49
62:Sf:103:LEU:HB2	62:Sf:105:TYR:CE1	2.48	0.49
67:SE:59:ASP:O	67:SE:63:LYS:HG3	2.12	0.49
78:SY:18:LEU:HB3	78:SY:20:ARG:HD3	1.95	0.49
82:S2:993:G:OP1	82:S2:1131:G:N2	2.38	0.49
1:Pt:9:A:O2'	1:Pt:10:G:N7	2.37	0.49
2:L5:197:A:N1	2:L5:225:G:O2'	2.39	0.49
2:L5:444:G:H2'	2:L5:445:U:C6	2.47	0.49
2:L5:2018:C:H2'	2:L5:2019:C:C6	2.46	0.49
2:L5:4066:U:H2'	2:L5:4067:U:H6	1.77	0.49
6:LB:36:ASP:N	6:LB:36:ASP:OD1	2.45	0.49
7:LC:8:ILE:HG23	7:LC:149:GLU:HG2	1.95	0.49
52:SM:117:GLU:O	52:SM:121:LYS:NZ	2.46	0.49
55:SR:60:ARG:NH1	82:S2:1464:C:O3'	2.46	0.49
63:Sg:22:ALA:HB1	63:Sg:71:ILE:HG23	1.94	0.49
63:Sg:230:LEU:HD21	63:Sg:259:TRP:CE2	2.48	0.49
70:SI:25:ARG:HA	82:S2:448:A:H5''	1.95	0.49
82:S2:382:C:H2'	82:S2:383:G:C8	2.47	0.49
82:S2:1628:C:H2'	82:S2:1629:C:C6	2.47	0.49
2:L5:1985:G:N2	2:L5:2003:G:HO2'	2.11	0.49
2:L5:3861:A:H2'	2:L5:3862:A:H8	1.78	0.49
21:LR:90:PRO:HB2	21:LR:93:VAL:HG23	1.95	0.49
28:LY:56:GLN:HG2	28:LY:67:ILE:HD13	1.95	0.49
40:Lk:54:GLU:OE2	40:Lk:58:GLN:NE2	2.37	0.49
52:SM:24:THR:HA	52:SM:27:ILE:HG12	1.95	0.49
58:SU:51:LYS:HG2	58:SU:90:ASP:HB2	1.94	0.49
58:SU:70:CYS:SG	82:S2:1491:G:O2'	2.64	0.49
62:Sf:107:LYS:O	62:Sf:115:SER:OG	2.24	0.49
80:Sb:68:GLY:O	82:S2:928:G:N2	2.43	0.49
82:S2:982:G:H2'	82:S2:983:A:H8	1.76	0.49
82:S2:1804:U:H2'	82:S2:1805:G:C8	2.48	0.49
2:L5:318:A:H2'	2:L5:319:A:H8	1.78	0.48
2:L5:457:G:H2'	2:L5:458:C:H6	1.77	0.48
2:L5:1095:A:N1	2:L5:1200:G:C6	2.80	0.48
2:L5:1824:G:H2'	2:L5:1825:A:C8	2.48	0.48
2:L5:2072:C:OP1	20:LQ:2:GLY:N	2.46	0.48
6:LB:29:VAL:HG12	6:LB:31:SER:H	1.78	0.48
14:LJ:35:ARG:O	14:LJ:39:VAL:HG23	2.13	0.48
16:LM:96:GLU:O	16:LM:100:ARG:HG2	2.13	0.48
16:LM:100:ARG:HA	16:LM:103:LYS:HE3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LW:73:ARG:NH2	82:S2:1749:G:O6	2.32	0.48
52:SM:86:GLY:HA2	52:SM:89:VAL:HG12	1.94	0.48
63:Sg:207:CYS:SG	63:Sg:219:TRP:HB2	2.53	0.48
66:SC:104:ASP:OD1	66:SC:105:GLU:N	2.46	0.48
76:SW:6:VAL:HG12	76:SW:34:ILE:HD11	1.95	0.48
82:S2:43:U:OP2	82:S2:485:A:N6	2.33	0.48
2:L5:10:A:H2'	2:L5:11:G:C8	2.48	0.48
2:L5:937:U:OP1	16:LM:46:ARG:NE	2.43	0.48
2:L5:2072:C:H5''	10:LF:116:GLN:HE21	1.77	0.48
2:L5:2486:G:O6	2:L5:2493:G:O6	2.31	0.48
3:L7:83:A:O2'	3:L7:85:G:OP1	2.30	0.48
17:LN:157:LYS:O	17:LN:162:ARG:NH1	2.45	0.48
21:LR:172:ARG:HH22	82:S2:909:G:P	2.35	0.48
50:SF:175:ASP:OD1	50:SF:179:ASN:ND2	2.46	0.48
51:SK:15:LEU:HD21	51:SK:71:LEU:HD21	1.95	0.48
51:SK:25:LYS:NZ	82:S2:1497:G:O6	2.34	0.48
53:SP:27:ASP:OD1	53:SP:27:ASP:N	2.44	0.48
61:Sd:8:TRP:HZ3	82:S2:1512:C:H5''	1.78	0.48
65:SB:120:MET:HE1	82:S2:987:A:C6	2.48	0.48
69:SH:42:GLU:HG2	69:SH:43:LEU:HD22	1.95	0.48
82:S2:146:G:H2'	82:S2:147:A:C8	2.48	0.48
82:S2:1010:G:H2'	82:S2:1011:A:H8	1.76	0.48
83:Zt:69:G:H2'	83:Zt:70:G:C8	2.47	0.48
2:L5:161:G:H2'	2:L5:162:A:H8	1.78	0.48
2:L5:418:A:C2	4:L8:17:A:H1'	2.48	0.48
2:L5:907:C:H2'	2:L5:908:G:C8	2.48	0.48
2:L5:1754:U:H1'	8:LD:3:PHE:HZ	1.78	0.48
2:L5:4563:U:H2'	2:L5:4564:A:H8	1.78	0.48
65:SB:99:ASN:OD1	65:SB:100:PHE:N	2.47	0.48
83:Zt:30:G:H2'	83:Zt:31:A:C8	2.46	0.48
2:L5:68:U:OP1	17:LN:178:HIS:ND1	2.45	0.48
2:L5:369:G:N2	2:L5:372:A:OP2	2.44	0.48
2:L5:2647:A:H3'	2:L5:2648:G:H8	1.78	0.48
2:L5:4909:A:H8	6:LB:156:TYR:CE2	2.32	0.48
46:Lr:26:SER:OG	46:Lr:28:GLU:OE1	2.23	0.48
47:Ls:24:TYR:HA	47:Ls:92:LYS:HZ3	1.78	0.48
65:SB:143:THR:HB	65:SB:205:TYR:HE2	1.79	0.48
65:SB:150:ILE:HD12	82:S2:1124:C:H5''	1.96	0.48
66:SC:95:ASP:OD1	66:SC:96:PHE:N	2.47	0.48
70:SI:25:ARG:NH2	82:S2:434:G:OP2	2.42	0.48
79:Sa:2:THR:N	82:S2:1199:A:OP1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:656:G:H5'	82:S2:662:G:N2	2.27	0.48
82:S2:1275:G:N2	82:S2:1506:A:OP2	2.38	0.48
82:S2:1667:U:H2'	82:S2:1668:U:C6	2.49	0.48
2:L5:928:C:H2'	2:L5:929:A:C8	2.49	0.48
2:L5:1993:C:H2'	2:L5:1994:C:C6	2.49	0.48
2:L5:2863:G:O2'	21:LR:82:LYS:O	2.30	0.48
5:LA:20:VAL:HA	5:LA:23:ARG:HG3	1.95	0.48
14:LJ:175:LEU:HD12	14:LJ:176:PRO:HD2	1.95	0.48
18:LO:54:TYR:HD2	18:LO:145:VAL:HG21	1.77	0.48
29:LZ:36:ARG:NH1	29:LZ:38:TYR:OH	2.37	0.48
57:ST:143:LYS:HG3	57:ST:144:LYS:HG2	1.96	0.48
74:SO:53:ILE:HG23	74:SO:88:LEU:HD13	1.96	0.48
82:S2:920:A:O2'	82:S2:922:A:O5'	2.32	0.48
2:L5:398:A2M:O5'	2:L5:398:A2M:H8	2.14	0.48
2:L5:691:C:H2'	2:L5:692:A:H8	1.79	0.48
2:L5:1846:G:H2'	2:L5:1847:C:H6	1.76	0.48
2:L5:3748:A:O2'	5:LA:223:SER:OG	2.27	0.48
2:L5:4600:G:H4'	2:L5:4601:U:O5'	2.13	0.48
2:L5:4680:G:H2'	2:L5:4681:A:C8	2.48	0.48
4:L8:153:C:H2'	4:L8:154:G:H8	1.78	0.48
6:LB:92:TYR:HB3	6:LB:99:LEU:HD22	1.96	0.48
34:Le:89:LEU:HD13	34:Le:118:LEU:HD22	1.95	0.48
49:SD:8:LYS:HG2	58:SU:61:LEU:HD11	1.95	0.48
52:SM:17:ALA:O	52:SM:20:GLU:HG3	2.14	0.48
55:SR:57:LEU:O	55:SR:61:ILE:HG12	2.13	0.48
65:SB:25:PHE:HD1	65:SB:28:LYS:HG3	1.77	0.48
82:S2:49:C:H2'	82:S2:472:C:H41	1.78	0.48
82:S2:895:G:H2'	82:S2:896:U:H4'	1.96	0.48
82:S2:1533:A:C8	82:S2:1604:G:H1'	2.48	0.48
83:Zt:15:G:N1	83:Zt:48:C:C2	2.82	0.48
2:L5:138:G:H2'	2:L5:139:G:H8	1.78	0.48
2:L5:226:G:N7	7:LC:184:TYR:OH	2.42	0.48
2:L5:918:G:H5'	16:LM:72:TYR:CZ	2.48	0.48
5:LA:225:ILE:HG12	5:LA:234:LYS:HA	1.96	0.48
7:LC:141:GLY:O	7:LC:204:ARG:NH1	2.34	0.48
16:LM:29:ASP:OD1	16:LM:30:VAL:N	2.45	0.48
57:ST:25:SER:HG	57:ST:27:LYS:HZ3	1.56	0.48
59:SZ:63:PRO:HG3	59:SZ:91:LEU:HD21	1.96	0.48
67:SE:31:PRO:HA	67:SE:81:THR:HB	1.95	0.48
68:SG:182:PRO:O	68:SG:186:GLN:HG2	2.14	0.48
69:SH:130:LEU:HG	69:SH:177:TYR:CE2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sa:59:PHE:HB2	79:Sa:62:TYR:HB2	1.95	0.48
82:S2:368:U:OP1	82:S2:369:C:O2'	2.32	0.48
2:L5:419:A:N3	2:L5:1332:C:O2'	2.42	0.48
2:L5:3811:G:O2'	2:L5:3814:U:OP2	2.31	0.48
2:L5:4156:G:H5''	2:L5:4157:A:H2'	1.96	0.48
2:L5:4761:G:OP2	18:LO:37:ARG:NH1	2.42	0.48
2:L5:4935:C:H2'	2:L5:4936:G:H8	1.78	0.48
7:LC:325:MET:HE1	10:LF:155:TYR:CZ	2.49	0.48
47:Ls:10:LYS:HB2	47:Ls:60:MET:HE1	1.94	0.48
50:SF:19:LEU:HD11	50:SF:50:PRO:HD3	1.95	0.48
55:SR:98:VAL:HG21	55:SR:117:LEU:HD22	1.95	0.48
63:Sg:228:TYR:CZ	63:Sg:264:LYS:HG2	2.49	0.48
64:SA:200:ASP:HA	64:SA:203:PHE:CE2	2.49	0.48
68:SG:174:PRO:HG3	82:S2:65:C:C2	2.48	0.48
72:SL:75:GLY:HA3	72:SL:88:ILE:HD12	1.95	0.48
79:Sa:32:LYS:NZ	82:S2:989:C:O2'	2.36	0.48
82:S2:1438:A:H2'	82:S2:1439:A:H8	1.79	0.48
2:L5:1241:C:O2'	31:Lb:120:ARG:O	2.32	0.48
2:L5:1327:C:H2'	2:L5:1328:G:C8	2.49	0.48
2:L5:1806:G:H2'	2:L5:1807:C:H6	1.77	0.48
2:L5:1998:A:O2'	2:L5:1999:A:O4'	2.25	0.48
2:L5:2558:C:H2'	2:L5:2559:G:C8	2.48	0.48
2:L5:2724:G:O2'	2:L5:2726:G:OP2	2.30	0.48
2:L5:2870:A:H2'	2:L5:2871:A:C8	2.49	0.48
2:L5:4492:U:O2'	2:L5:4512:U:O2	2.25	0.48
11:LG:153:GLN:N	11:LG:204:PHE:O	2.44	0.48
24:LU:21:PHE:N	24:LU:72:VAL:O	2.42	0.48
24:LU:33:ILE:HD12	24:LU:96:LEU:HD13	1.95	0.48
33:Ld:114:PHE:HA	33:Ld:117:LEU:HD12	1.96	0.48
50:SF:126:THR:HA	50:SF:135:ARG:HG3	1.96	0.48
63:Sg:159:ASN:HD21	63:Sg:161:SER:HB2	1.79	0.48
63:Sg:197:THR:HG21	63:Sg:238:ALA:HA	1.96	0.48
65:SB:36:PRO:HB3	65:SB:231:LEU:HG	1.96	0.48
66:SC:191:VAL:HG11	66:SC:236:PHE:HA	1.94	0.48
80:Sb:49:HIS:ND1	80:Sb:69:GLY:O	2.47	0.48
82:S2:564:A:H62	82:S2:586:G:H21	1.61	0.48
2:L5:965:G:H21	2:L5:2092:G:H1'	1.79	0.48
2:L5:1563:A:N6	82:S2:1028:A:N1	2.62	0.48
2:L5:1960:A:C8	47:Ls:63:LYS:HE3	2.49	0.48
2:L5:2376:A:H2'	2:L5:2377:C:C6	2.49	0.48
2:L5:2754:G:OP2	29:LZ:133:LYS:NZ	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4095:G:H2'	2:L5:4096:C:C6	2.49	0.48
6:LB:27:GLY:HA2	6:LB:276:HIS:CD2	2.49	0.48
58:SU:49:LYS:HE2	58:SU:92:HIS:ND1	2.29	0.48
64:SA:155:ARG:NH2	82:S2:1137:U:O3'	2.47	0.48
64:SA:169:HIS:HA	64:SA:203:PHE:CD1	2.49	0.48
66:SC:205:VAL:O	66:SC:224:THR:OG1	2.28	0.48
82:S2:186:C:H2'	82:S2:187:G:C8	2.49	0.48
82:S2:1562:C:H2'	82:S2:1563:G:H8	1.79	0.48
2:L5:1346:C:H2'	2:L5:1347:G:H8	1.79	0.47
2:L5:2361:G:O2'	2:L5:3859:G:O6	2.30	0.47
6:LB:219:VAL:HG11	6:LB:337:VAL:HG13	1.95	0.47
17:LN:46:ASP:OD1	17:LN:47:LYS:N	2.47	0.47
30:La:63:LEU:HD22	30:La:65:ARG:HH11	1.78	0.47
35:Lf:36:ARG:NH1	35:Lf:79:GLY:O	2.43	0.47
49:SD:138:VAL:HB	49:SD:150:MET:HE3	1.96	0.47
60:Sc:13:ARG:HB2	60:Sc:55:VAL:HG12	1.96	0.47
68:SG:31:ARG:HG3	68:SG:101:ILE:HG22	1.95	0.47
82:S2:656:G:N2	82:S2:663:C:H5''	2.29	0.47
82:S2:1731:A:H2'	82:S2:1732:G:C8	2.49	0.47
2:L5:268:G:H2'	2:L5:269:G:C8	2.48	0.47
2:L5:2638:G:H22	2:L5:2719:C:P	2.36	0.47
2:L5:3606:U:H2'	2:L5:3607:U:C6	2.48	0.47
2:L5:3867:A2M:H2'	2:L5:3868:G:O4'	2.13	0.47
2:L5:4188:U:H2'	2:L5:4189:U:C6	2.49	0.47
2:L5:4227:OMU:HM23	2:L5:4227:OMU:H1'	1.70	0.47
15:LL:100:PRO:O	38:Li:25:ARG:NH2	2.47	0.47
18:LO:88:LEU:HD12	18:LO:99:LEU:HD13	1.97	0.47
29:LZ:57:MET:HB3	29:LZ:61:LYS:HD3	1.96	0.47
53:SP:76:VAL:O	53:SP:95:GLY:N	2.32	0.47
57:ST:25:SER:OG	57:ST:27:LYS:NZ	2.29	0.47
59:SZ:42:ASP:OD1	59:SZ:43:LYS:N	2.43	0.47
61:Sd:2:GLY:HA3	61:Sd:6:LEU:HD11	1.95	0.47
64:SA:70:ASN:HB3	64:SA:73:ASP:OD2	2.14	0.47
65:SB:40:ASN:OD1	65:SB:41:ILE:HD12	2.14	0.47
79:Sa:60:ASP:OD1	79:Sa:60:ASP:N	2.42	0.47
79:Sa:66:LYS:HB2	79:Sa:68:TYR:CE1	2.49	0.47
2:L5:959:G:C8	9:LE:123:ARG:HG2	2.50	0.47
2:L5:1333:A:H2'	2:L5:1334:A:H8	1.79	0.47
2:L5:1698:C:H5''	2:L5:1699:A:O4'	2.14	0.47
2:L5:1989:G:H2'	2:L5:1990:A:C8	2.49	0.47
2:L5:4467:A:O2'	2:L5:4510:A:N3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4627:U:O2'	6:LB:55:HIS:ND1	2.41	0.47
6:LB:293:ILE:HG12	6:LB:297:LYS:HG2	1.94	0.47
6:LB:302:ASN:HB2	6:LB:313:SER:HA	1.95	0.47
6:LB:317:LEU:HB3	6:LB:372:SER:HB2	1.96	0.47
8:LD:206:ASP:OD1	8:LD:209:ARG:NH2	2.48	0.47
24:LU:23:LEU:HB2	24:LU:70:ILE:HB	1.96	0.47
34:Le:117:GLN:O	46:Lr:119:ARG:NH2	2.45	0.47
62:Sf:130:VAL:HG11	62:Sf:143:LYS:HZ3	1.79	0.47
64:SA:104:THR:O	64:SA:107:THR:OG1	2.31	0.47
68:SG:159:ARG:HH21	68:SG:171:THR:HG23	1.78	0.47
71:SJ:39:ASN:HB2	82:S2:642:U:P	2.53	0.47
82:S2:379:C:H2'	82:S2:380:G:C8	2.49	0.47
82:S2:898:U:C4	82:S2:900:C:C4	3.02	0.47
82:S2:1288:OMU:HN3	82:S2:1311:C:H42	1.62	0.47
82:S2:1501:C:H2'	82:S2:1502:C:H6	1.79	0.47
2:L5:83:C:O2'	2:L5:100:C:N4	2.47	0.47
2:L5:192:G:H2'	2:L5:193:G:H8	1.79	0.47
2:L5:1095:A:H2	2:L5:1200:G:N1	2.11	0.47
2:L5:1971:C:O2	47:Ls:41:GLN:NE2	2.47	0.47
2:L5:3848:U:H2'	2:L5:3849:A:C8	2.49	0.47
2:L5:3869:OMC:C2	86:L5:5294:SPM:H32	2.49	0.47
2:L5:4093:G:H1	2:L5:4114:C:H2'	1.80	0.47
7:LC:291:ARG:HH21	46:Lr:46:ARG:HH12	1.61	0.47
7:LC:298:ILE:HD13	20:LQ:131:PRO:HB3	1.97	0.47
8:LD:83:LEU:HB3	8:LD:88:VAL:HG13	1.95	0.47
8:LD:89:LYS:HE2	8:LD:229:ASN:HB2	1.95	0.47
46:Lr:28:GLU:OE2	46:Lr:31:ASN:ND2	2.37	0.47
53:SP:56:LEU:HD22	53:SP:83:MET:HE2	1.96	0.47
54:SQ:110:ASP:N	54:SQ:110:ASP:OD1	2.46	0.47
57:ST:77:LYS:NZ	82:S2:1584:G:OP1	2.47	0.47
63:Sg:133:ASN:HB3	63:Sg:139:LYS:HD2	1.97	0.47
65:SB:126:ASP:OD1	65:SB:136:ARG:NE	2.37	0.47
66:SC:68:ARG:HG2	66:SC:277:HIS:HB2	1.95	0.47
76:SW:76:SER:OG	82:S2:1158:G:O3'	2.30	0.47
2:L5:93:G:H2'	2:L5:94:A:C8	2.50	0.47
2:L5:713:C:H2'	2:L5:714:G:H8	1.79	0.47
2:L5:2341:A:OP2	30:La:4:ARG:NH2	2.45	0.47
2:L5:2407:G:OP2	2:L5:2407:G:N2	2.42	0.47
2:L5:2811:G:N1	2:L5:2814:C:OP2	2.41	0.47
2:L5:4113:U:H4'	2:L5:4115:G:C5	2.49	0.47
2:L5:4743:G:H2'	2:L5:4744:A:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LL:59:VAL:HG21	15:LL:73:GLY:HA3	1.95	0.47
40:Lk:68:GLU:HG3	40:Lk:70:LYS:H	1.78	0.47
64:SA:57:LYS:NZ	64:SA:160:ALA:O	2.43	0.47
76:SW:69:LEU:HD21	76:SW:72:CYS:HB3	1.95	0.47
82:S2:634:A:H2'	82:S2:635:G:H8	1.79	0.47
82:S2:835:C:H4'	82:S2:836:G:H8	1.79	0.47
82:S2:1222:G:H2'	82:S2:1223:A:C8	2.50	0.47
82:S2:1681:U:H2'	82:S2:1682:C:C6	2.50	0.47
2:L5:422:C:H2'	2:L5:423:G:C8	2.49	0.47
2:L5:444:G:H2'	2:L5:445:U:H6	1.80	0.47
2:L5:491:G:H2'	2:L5:492:U:C6	2.50	0.47
2:L5:1070:G:O2'	2:L5:1071:C:O5'	2.33	0.47
2:L5:1186:U:H2'	2:L5:1187:G:N3	2.29	0.47
2:L5:1323:A2M:HM'3	2:L5:1323:A2M:H1'	1.63	0.47
2:L5:1348:U:H2'	2:L5:1349:G:H8	1.80	0.47
2:L5:2436:U:H3'	27:LX:127:LEU:HD22	1.95	0.47
2:L5:4281:A:H2'	2:L5:4282:A:H2'	1.95	0.47
5:LA:48:ILE:HG22	45:Lp:54:ILE:HG12	1.97	0.47
7:LC:33:ARG:NH2	7:LC:35:ASP:OD2	2.48	0.47
8:LD:211:LEU:HD12	8:LD:223:PHE:HE2	1.78	0.47
17:LN:159:ARG:HB3	17:LN:164:LEU:HB2	1.95	0.47
32:Lc:79:ILE:HD13	32:Lc:90:ARG:HG2	1.97	0.47
49:SD:172:VAL:HG22	49:SD:185:LYS:HG2	1.97	0.47
55:SR:104:GLU:HA	55:SR:107:LYS:HG2	1.97	0.47
64:SA:42:LYS:HB3	64:SA:44:ASP:H	1.80	0.47
67:SE:48:LEU:HD23	67:SE:52:LEU:HD12	1.97	0.47
82:S2:1189:A:H2'	82:S2:1190:A:C8	2.49	0.47
82:S2:1457:U:H2'	82:S2:1458:G:H8	1.78	0.47
83:Zt:19:G:O2'	83:Zt:48:C:N4	2.32	0.47
83:Zt:28:C:H2'	83:Zt:29:A:H8	1.79	0.47
2:L5:44:A:H5''	86:L5:5264:SPM:H81	1.97	0.47
2:L5:702:U:H2'	2:L5:703:G:O4'	2.14	0.47
2:L5:1239:C:H5	9:LE:60:SER:HB2	1.79	0.47
2:L5:1269:G:O2'	2:L5:1270:A:O4'	2.30	0.47
2:L5:2658:G:O2'	2:L5:2675:G:N2	2.48	0.47
2:L5:3855:C:H2'	2:L5:3856:A:H8	1.80	0.47
2:L5:3861:A:H2'	2:L5:3862:A:C8	2.49	0.47
2:L5:4523:A2M:H1'	2:L5:4558:U:C4	2.50	0.47
2:L5:4524:G:C2	6:LB:252:ALA:HB1	2.50	0.47
2:L5:4929:C:H5''	16:LM:114:LYS:HD2	1.97	0.47
7:LC:294:LYS:HA	7:LC:299:GLN:HE21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LD:164:LYS:HG2	8:LD:195:HIS:CE1	2.49	0.47
11:LG:105:GLU:OE1	11:LG:105:GLU:N	2.36	0.47
20:LQ:112:ARG:HG2	20:LQ:115:ARG:HH21	1.79	0.47
20:LQ:155:ALA:O	20:LQ:158:THR:OG1	2.27	0.47
23:LT:4:THR:O	23:LT:9:ARG:NE	2.47	0.47
23:LT:116:LYS:O	23:LT:120:LYS:HG2	2.15	0.47
45:Lp:27:LYS:O	45:Lp:31:ILE:HG12	2.15	0.47
45:Lp:85:ARG:HH22	82:S2:939:U:P	2.38	0.47
48:Lt:44:ASP:OD1	48:Lt:45:ASP:N	2.47	0.47
50:SF:22:LYS:NZ	50:SF:98:GLU:OE2	2.35	0.47
51:SK:29:MET:HE2	51:SK:31:LYS:O	2.14	0.47
55:SR:84:TYR:CE2	64:SA:213:GLU:HG3	2.50	0.47
56:SS:38:ARG:O	56:SS:42:HIS:ND1	2.33	0.47
57:ST:91:HIS:NE2	82:S2:1665:G:OP1	2.48	0.47
59:SZ:62:VAL:HA	59:SZ:65:TYR:CE1	2.50	0.47
63:Sg:89:LEU:HG	63:Sg:101:PHE:HE1	1.78	0.47
65:SB:155:TYR:OH	82:S2:989:C:OP2	2.23	0.47
68:SG:7:PHE:CZ	68:SG:9:ALA:HB3	2.50	0.47
71:SJ:35:TYR:HD2	71:SJ:106:LEU:HD13	1.80	0.47
72:SL:130:GLU:OE2	82:S2:351:G:N2	2.46	0.47
76:SW:106:THR:OG1	76:SW:122:GLY:O	2.25	0.47
81:Se:37:GLN:HB3	81:Se:41:ARG:HH12	1.77	0.47
82:S2:576:A2M:HM'3	82:S2:576:A2M:H1'	1.70	0.47
82:S2:693:A:H2	82:S2:739:C:H4'	1.79	0.47
82:S2:698:G:H2'	82:S2:733:C:C4	2.50	0.47
82:S2:1037:G:H4'	82:S2:1845:A:H4'	1.95	0.47
82:S2:1220:A:H2'	82:S2:1221:G:O4'	2.15	0.47
82:S2:1253:A:H4'	82:S2:1254:C:H5''	1.96	0.47
82:S2:1801:A:H2'	82:S2:1802:C:C6	2.49	0.47
83:Zt:22:G:H2'	83:Zt:23:A:H8	1.79	0.47
1:Pt:1:G:H21	13:LI:111:LEU:HD22	1.80	0.47
2:L5:1236:C:H2'	2:L5:1237:C:C6	2.49	0.47
2:L5:1994:C:H2'	2:L5:1995:G:H8	1.75	0.47
2:L5:2275:G:H2'	2:L5:2276:A:C8	2.50	0.47
2:L5:2693:G:OP2	40:Lk:33:LYS:NZ	2.41	0.47
2:L5:3796:U:HO2'	82:S2:1720:U:HO2'	1.56	0.47
9:LE:128:HIS:ND1	9:LE:128:HIS:O	2.48	0.47
19:LP:16:LYS:HG2	19:LP:149:ILE:HG12	1.96	0.47
20:LQ:86:ILE:HD11	20:LQ:100:VAL:HG11	1.96	0.47
26:LW:92:ALA:O	26:LW:96:GLN:NE2	2.47	0.47
37:Lh:91:MET:HG3	37:Lh:94:ARG:NH1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SQ:13:PHE:HA	54:SQ:22:VAL:HA	1.97	0.47
54:SQ:37:ARG:NH2	82:S2:1543:U:OP1	2.37	0.47
56:SS:45:LEU:HD22	56:SS:50:ILE:HG21	1.96	0.47
67:SE:146:THR:HG21	82:S2:122:G:H21	1.80	0.47
78:SY:76:TYR:OH	78:SY:86:GLU:OE1	2.22	0.47
82:S2:557:U:H2'	82:S2:558:G:C8	2.50	0.47
82:S2:1407:U:H2'	82:S2:1408:U:C6	2.49	0.47
1:Pt:58:A:O2'	1:Pt:61:C:N4	2.48	0.47
2:L5:142:G:O2'	2:L5:144:G:O5'	2.28	0.47
2:L5:710:G:H2'	2:L5:711:A:C8	2.49	0.47
2:L5:928:C:H2'	2:L5:929:A:H8	1.79	0.47
2:L5:1995:G:H2'	2:L5:1996:C:C6	2.50	0.47
2:L5:3610:A:H2'	2:L5:3611:A:H8	1.80	0.47
2:L5:3870:C:H2'	2:L5:3871:A:C8	2.50	0.47
2:L5:3910:C:H2'	2:L5:3911:C:C6	2.50	0.47
2:L5:3928:A:H2'	2:L5:3929:G:O4'	2.14	0.47
2:L5:4076:G:OP1	11:LG:73:ARG:NE	2.47	0.47
2:L5:4358:U:H4'	15:LL:197:LYS:HD3	1.97	0.47
2:L5:4923:C:C4	2:L5:4924:C:N4	2.83	0.47
6:LB:147:GLU:CD	6:LB:198:ARG:HH22	2.22	0.47
17:LN:140:LYS:HD3	17:LN:140:LYS:HA	1.64	0.47
26:LW:91:MET:HA	26:LW:94:ARG:HG2	1.97	0.47
48:Lt:77:ALA:HB3	48:Lt:80:LEU:HB2	1.97	0.47
49:SD:66:ILE:HD11	49:SD:86:LEU:HB3	1.97	0.47
54:SQ:13:PHE:HB3	54:SQ:22:VAL:HG22	1.97	0.47
64:SA:184:ARG:NE	64:SA:191:ARG:HD3	2.29	0.47
65:SB:145:LYS:HE3	65:SB:145:LYS:HB2	1.69	0.47
66:SC:64:THR:HG22	66:SC:66:LEU:H	1.80	0.47
1:Pt:27:U:H2'	1:Pt:28:U:C6	2.50	0.47
2:L5:687:U:N3	9:LE:95:PRO:HG2	2.30	0.47
2:L5:1307:A:H2'	2:L5:1308:C:C6	2.50	0.47
2:L5:1734:G:N2	2:L5:1735:U:O4	2.45	0.47
2:L5:1836:G:O5'	23:LT:129:LYS:NZ	2.47	0.47
2:L5:2298:U:OP1	7:LC:204:ARG:NE	2.47	0.47
2:L5:2749:C:H2'	2:L5:2750:G:C8	2.50	0.47
2:L5:2822:G:N7	21:LR:20:LYS:NZ	2.54	0.47
2:L5:4504:C:H2'	2:L5:4505:C:C6	2.50	0.47
2:L5:4883:C:N4	9:LE:181:LEU:O	2.39	0.47
4:L8:67:U:H2'	4:L8:68:G:C8	2.50	0.47
5:LA:142:GLU:OE2	65:SB:222:LYS:NZ	2.48	0.47
7:LC:4:ALA:O	7:LC:29:LYS:NZ	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LD:271:MET:HE3	8:LD:276:LYS:HG2	1.97	0.47
9:LE:157:HIS:HA	9:LE:160:LYS:HE3	1.97	0.47
26:LW:80:ARG:NH2	68:SG:8:PRO:O	2.48	0.47
50:SF:22:LYS:HG3	50:SF:23:TRP:CD2	2.50	0.47
53:SP:83:MET:HE3	53:SP:116:LEU:HD11	1.97	0.47
54:SQ:18:THR:OG1	82:S2:1672:U:OP1	2.33	0.47
57:ST:30:VAL:HG22	57:ST:53:PHE:HD2	1.79	0.47
63:Sg:66:VAL:HG22	63:Sg:82:SER:HB2	1.97	0.47
65:SB:39:PHE:CE1	65:SB:189:ILE:HD11	2.49	0.47
70:SI:3:ILE:O	70:SI:30:GLY:N	2.47	0.47
73:SN:115:LEU:HA	73:SN:118:ILE:HG22	1.96	0.47
77:SX:28:LYS:O	77:SX:32:LEU:HB2	2.15	0.47
82:S2:656:G:H21	82:S2:663:C:H5''	1.80	0.47
82:S2:1714:U:H2'	82:S2:1715:A:C8	2.49	0.47
82:S2:1777:G:H2'	82:S2:1778:C:C6	2.48	0.47
2:L5:494:U:H2'	2:L5:495:C:C6	2.50	0.46
2:L5:956:A:H1'	2:L5:2076:G:H5''	1.97	0.46
2:L5:2654:C:H2'	2:L5:2655:C:H6	1.80	0.46
2:L5:4611:A:H2'	2:L5:4612:C:H6	1.80	0.46
9:LE:131:LYS:O	9:LE:136:HIS:NE2	2.47	0.46
15:LL:48:PRO:HB2	37:Lh:120:ALA:HB2	1.98	0.46
15:LL:64:VAL:HA	15:LL:67:HIS:CD2	2.36	0.46
15:LL:145:LYS:HG3	15:LL:146:LEU:HD12	1.97	0.46
55:SR:59:LYS:NZ	82:S2:1456:G:OP1	2.42	0.46
57:ST:30:VAL:HG22	57:ST:53:PHE:CD2	2.50	0.46
57:ST:62:ARG:NH2	82:S2:1543:U:OP2	2.34	0.46
63:Sg:216:ALA:N	63:Sg:230:LEU:O	2.48	0.46
63:Sg:245:ARG:HB3	63:Sg:247:TRP:CE3	2.50	0.46
75:SV:66:ASP:OD1	75:SV:67:ASP:N	2.47	0.46
82:S2:440:G:OP1	82:S2:1798:C:O2'	2.27	0.46
82:S2:549:C:H2'	82:S2:550:C:C6	2.51	0.46
82:S2:1755:C:H2'	82:S2:1756:C:C6	2.50	0.46
82:S2:1801:A:H2'	82:S2:1802:C:H6	1.80	0.46
2:L5:315:G:C8	30:La:62:HIS:HB2	2.50	0.46
2:L5:3785:A2M:H2	2:L5:4551:U:O2	2.15	0.46
2:L5:4069:U:H2'	2:L5:4070:U:C6	2.50	0.46
24:LU:99:TRP:CZ3	84:CI:58:LEU:CA	2.94	0.46
27:LX:64:SER:OG	37:Lh:82:ASP:OD2	2.31	0.46
34:Le:100:ALA:HB3	34:Le:103:VAL:HG23	1.97	0.46
38:Li:76:ARG:HD3	38:Li:76:ARG:HA	1.74	0.46
47:Ls:99:ARG:HG3	47:Ls:103:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:Lt:112:ILE:HD12	48:Lt:115:GLN:HG3	1.97	0.46
59:SZ:55:TYR:O	59:SZ:58:LEU:HG	2.14	0.46
60:Sc:34:PHE:CD2	60:Sc:40:ARG:HD3	2.51	0.46
70:SI:191:GLU:HG3	72:SL:19:ASN:ND2	2.30	0.46
74:SO:147:ARG:HH22	82:S2:1854:U:P	2.37	0.46
82:S2:17:C:H2'	82:S2:18:C:C6	2.50	0.46
82:S2:1545:A:H2'	82:S2:1546:G:C8	2.50	0.46
82:S2:1856:C:H2'	82:S2:1857:G:H8	1.80	0.46
2:L5:1772:C:H2'	2:L5:1773:U:H6	1.80	0.46
2:L5:1779:U:H2'	2:L5:1780:A:C8	2.50	0.46
2:L5:2640:G:H2'	2:L5:2641:A:C8	2.51	0.46
2:L5:3911:C:H2'	2:L5:3912:U:C6	2.49	0.46
2:L5:4730:C:H2'	2:L5:4731:G:C8	2.51	0.46
9:LE:190:HIS:HB3	9:LE:193:PHE:HD2	1.81	0.46
32:Lc:34:THR:HG23	32:Lc:95:ALA:HB2	1.97	0.46
56:SS:44:VAL:HG21	56:SS:71:MET:HE1	1.96	0.46
63:Sg:59:LEU:HD23	63:Sg:90:TRP:CD2	2.50	0.46
66:SC:133:TYR:CE1	66:SC:216:MET:HA	2.49	0.46
69:SH:31:GLU:HA	69:SH:37:LYS:HG3	1.96	0.46
70:SI:101:ILE:HG22	70:SI:174:CYS:HB2	1.97	0.46
73:SN:64:ARG:NH1	82:S2:919:A:OP2	2.48	0.46
82:S2:436:OMG:OP2	82:S2:471:G:O2'	2.33	0.46
2:L5:181:C:H2'	2:L5:182:G:C8	2.50	0.46
2:L5:961:G:O6	9:LE:123:ARG:NH1	2.36	0.46
2:L5:1367:C:O2'	2:L5:1369:C:OP2	2.33	0.46
2:L5:1751:A:H2'	2:L5:1752:G:C8	2.51	0.46
2:L5:2465:C:H2'	2:L5:2466:G:O4'	2.16	0.46
2:L5:3687:A:O2'	5:LA:236:GLY:N	2.48	0.46
2:L5:3799:A:N3	2:L5:4506:C:O2'	2.43	0.46
3:L7:23:A:N3	3:L7:118:C:O2'	2.38	0.46
5:LA:112:ILE:HG22	5:LA:135:THR:HG23	1.97	0.46
8:LD:41:LYS:HG3	23:LT:93:ILE:HG21	1.98	0.46
14:LJ:115:LEU:O	14:LJ:117:ILE:HD12	2.15	0.46
47:Ls:20:LEU:HD11	47:Ls:52:VAL:HG11	1.97	0.46
49:SD:65:ARG:HA	49:SD:68:GLU:CD	2.40	0.46
67:SE:125:LYS:O	67:SE:142:HIS:N	2.49	0.46
69:SH:17:ASP:OD1	69:SH:17:ASP:N	2.48	0.46
69:SH:34:SER:OG	69:SH:78:ARG:NH2	2.38	0.46
69:SH:98:ARG:NH2	82:S2:913:A:N1	2.63	0.46
70:SI:114:GLU:OE2	70:SI:121:LEU:N	2.49	0.46
82:S2:323:C:H5'	82:S2:324:C:OP1	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:352:U:H2'	82:S2:353:C:C6	2.51	0.46
82:S2:532:C:H2'	82:S2:533:A:H8	1.80	0.46
2:L5:1077:C:OP1	2:L5:1215:C:O2'	2.30	0.46
2:L5:4364:G:H2'	2:L5:4365:C:H6	1.81	0.46
3:L7:7:G:H5''	8:LD:22:ARG:HD3	1.97	0.46
6:LB:59:GLU:HB2	6:LB:366:LYS:HE2	1.96	0.46
6:LB:216:MET:HE2	6:LB:281:ASN:HB3	1.97	0.46
15:LL:138:ASP:OD1	15:LL:139:SER:N	2.49	0.46
35:Lf:45:LYS:HD2	35:Lf:105:LEU:HA	1.97	0.46
54:SQ:37:ARG:HD3	54:SQ:41:MET:HE1	1.97	0.46
54:SQ:130:LYS:NZ	54:SQ:131:LYS:O	2.48	0.46
56:SS:68:ILE:O	56:SS:71:MET:N	2.49	0.46
56:SS:74:PRO:HG2	56:SS:84:LEU:HD21	1.98	0.46
61:Sd:22:ARG:HG2	61:Sd:38:MET:HG2	1.98	0.46
66:SC:209:VAL:HG21	66:SC:233:LEU:HD11	1.97	0.46
69:SH:23:ILE:HG12	69:SH:60:ILE:HD11	1.96	0.46
77:SX:119:ARG:HH22	82:S2:1192:U:P	2.39	0.46
82:S2:669:A:H2'	82:S2:670:A:C8	2.51	0.46
82:S2:1231:C:O2'	82:S2:1253:A:N6	2.48	0.46
82:S2:1323:U:H2'	82:S2:1324:G:C8	2.50	0.46
82:S2:1648:G:O2'	82:S2:1674:G:O6	2.25	0.46
83:Zt:45:G:H8	83:Zt:45:G:OP2	1.98	0.46
2:L5:1504:G:H2'	2:L5:1505:C:H6	1.81	0.46
2:L5:2634:C:H2'	2:L5:2635:U:C6	2.51	0.46
2:L5:2704:C:H2'	2:L5:2705:G:H8	1.79	0.46
2:L5:2870:A:H2'	2:L5:2871:A:H8	1.80	0.46
2:L5:3690:U:H2'	2:L5:3691:G:O4'	2.16	0.46
2:L5:3824:A:H2	45:Lp:16:THR:HG22	1.80	0.46
34:Le:90:MET:HG3	46:Lr:33:LYS:HA	1.98	0.46
59:SZ:69:THR:HB	59:SZ:72:VAL:HG22	1.96	0.46
62:Sf:94:LYS:HE3	62:Sf:94:LYS:HB3	1.73	0.46
63:Sg:4:GLN:O	63:Sg:313:THR:N	2.46	0.46
70:SI:121:LEU:HD21	70:SI:166:PHE:CE2	2.51	0.46
72:SL:13:GLN:HE22	72:SL:35:ARG:HA	1.81	0.46
82:S2:432:G:H2'	82:S2:433:A:C8	2.51	0.46
82:S2:647:U:H2'	82:S2:648:A:C8	2.49	0.46
82:S2:851:C:H5''	82:S2:852:G:H5'	1.97	0.46
1:Pt:3:C:H2'	1:Pt:4:U:H6	1.81	0.46
2:L5:1806:G:H2'	2:L5:1807:C:C6	2.50	0.46
2:L5:2079:G:H2'	2:L5:2080:U:C6	2.51	0.46
2:L5:2401:A2M:H5''	2:L5:2401:A2M:H8	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3684:G:H2'	2:L5:3685:C:C6	2.51	0.46
2:L5:4584:A:H2'	2:L5:4585:U:O4'	2.15	0.46
6:LB:163:ILE:HG22	6:LB:180:LEU:HD12	1.97	0.46
8:LD:150:LEU:HD12	14:LJ:146:ARG:HG3	1.97	0.46
9:LE:150:LEU:HD11	9:LE:164:PHE:HB2	1.98	0.46
11:LG:73:ARG:HD3	11:LG:73:ARG:HA	1.78	0.46
21:LR:105:LEU:HD23	21:LR:138:LEU:HD23	1.98	0.46
21:LR:151:ARG:NH2	72:SL:118:ARG:HD3	2.31	0.46
26:LW:4:GLU:HG2	26:LW:12:LYS:NZ	2.30	0.46
26:LW:82:ILE:HG12	68:SG:131:ARG:HG3	1.97	0.46
63:Sg:191:HIS:CD2	63:Sg:195:LEU:HD21	2.50	0.46
65:SB:122:GLU:HG2	65:SB:140:VAL:HG12	1.97	0.46
71:SJ:39:ASN:HA	81:Se:34:ARG:CZ	2.46	0.46
79:Sa:8:ASN:ND2	82:S2:1861:G:OP1	2.49	0.46
82:S2:24:C:H42	82:S2:650:A:H61	1.62	0.46
82:S2:199:C:H1'	82:S2:200:G:C8	2.51	0.46
82:S2:1657:G:H2'	82:S2:1658:G:H8	1.79	0.46
82:S2:1779:G:H2'	82:S2:1780:G:C8	2.50	0.46
83:Zt:48:C:C4	83:Zt:59:G:C5	3.03	0.46
1:Pt:51:C:H2'	1:Pt:52:G:H8	1.81	0.46
1:Pt:56:C:N4	44:Lo:104:ILE:HG21	2.30	0.46
2:L5:106:A:H2'	2:L5:107:G:O4'	2.16	0.46
2:L5:1299:G:H2'	2:L5:1300:G:H8	1.80	0.46
2:L5:3718:A2M:HM'3	2:L5:3718:A2M:H1'	1.67	0.46
86:L5:5289:SPM:HN0	86:L5:5289:SPM:H72	1.47	0.46
9:LE:132:PRO:HG2	9:LE:135:GLN:HG3	1.97	0.46
12:LH:41:ILE:HG22	12:LH:43:VAL:HG13	1.97	0.46
16:LM:47:ARG:NH2	16:LM:68:ALA:O	2.42	0.46
26:LW:5:LEU:HB3	26:LW:30:GLN:HG3	1.98	0.46
27:LX:107:HIS:O	27:LX:111:GLN:HG3	2.15	0.46
33:Ld:91:LYS:HE3	33:Ld:105:LEU:HD13	1.96	0.46
52:SM:63:LYS:HG3	52:SM:64:LEU:HD22	1.97	0.46
54:SQ:132:PHE:HD2	58:SU:79:ARG:HH21	1.64	0.46
67:SE:11:ARG:NH1	67:SE:24:THR:OG1	2.49	0.46
69:SH:82:GLU:O	69:SH:86:LYS:HG2	2.16	0.46
74:SO:134:PRO:HB3	82:S2:944:A:H5''	1.97	0.46
74:SO:141:ARG:NH2	82:S2:1856:C:OP1	2.46	0.46
82:S2:1101:U:H2'	82:S2:1102:G:H8	1.80	0.46
82:S2:1587:G:OP1	82:S2:1587:G:N2	2.48	0.46
82:S2:1617:G:N2	82:S2:1619:A:H3'	2.31	0.46
82:S2:1657:G:H2'	82:S2:1658:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1241:C:H5'	9:LE:72:LYS:NZ	2.31	0.46
2:L5:1617:G:H1'	2:L5:2513:A:N6	2.31	0.46
2:L5:1974:U:O3'	2:L5:1975:G:H3'	2.15	0.46
2:L5:1974:U:H3	2:L5:1993:C:H42	1.64	0.46
2:L5:3748:A:HO2'	5:LA:223:SER:HG	1.58	0.46
2:L5:3925:OMU:H4'	44:Lo:51:GLN:HB3	1.98	0.46
2:L5:4067:U:H2'	2:L5:4068:U:C6	2.51	0.46
2:L5:4122:G:O3'	36:Lg:90:ARG:NH2	2.49	0.46
2:L5:4196:OMG:HM23	2:L5:4196:OMG:H1'	1.69	0.46
21:LR:13:SER:OG	21:LR:38:ARG:NH1	2.49	0.46
41:Ll:23:ILE:HG23	41:Ll:38:ASN:HB2	1.97	0.46
53:SP:57:LEU:HB3	53:SP:61:ARG:HH12	1.80	0.46
63:Sg:27:PHE:HB2	63:Sg:30:MET:HE3	1.98	0.46
63:Sg:82:SER:OG	63:Sg:83:TRP:N	2.48	0.46
64:SA:145:ILE:HG23	64:SA:159:ILE:HB	1.98	0.46
67:SE:18:TRP:CH2	67:SE:31:PRO:HD3	2.50	0.46
69:SH:144:ILE:O	76:SW:52:ILE:N	2.37	0.46
70:SI:121:LEU:HD11	70:SI:166:PHE:HD2	1.81	0.46
82:S2:694:G:H5''	82:S2:730:C:H41	1.81	0.46
82:S2:1146:C:O2'	82:S2:1150:A:N1	2.47	0.46
2:L5:1759:G:N2	2:L5:1773:U:O2	2.37	0.46
2:L5:4244:A:H2'	2:L5:4245:G:O4'	2.16	0.46
2:L5:4530:UR3:O5'	2:L5:4530:UR3:H6	2.16	0.46
4:L8:66:A:H2'	4:L8:67:U:C6	2.51	0.46
4:L8:89:U:H2'	4:L8:90:C:C6	2.51	0.46
10:LF:46:ARG:O	10:LF:50:ILE:HG12	2.16	0.46
14:LJ:17:ILE:HD12	14:LJ:132:VAL:HG21	1.98	0.46
16:LM:77:TRP:O	16:LM:81:ASP:HA	2.16	0.46
33:Ld:48:GLU:O	33:Ld:51:LYS:HG3	2.16	0.46
47:Ls:28:PHE:CE2	47:Ls:192:VAL:HG12	2.51	0.46
52:SM:36:ARG:HG3	52:SM:40:LYS:NZ	2.31	0.46
54:SQ:93:VAL:HG21	54:SQ:120:LEU:HD11	1.98	0.46
61:Sd:32:ARG:NH1	82:S2:1661:A:OP2	2.36	0.46
63:Sg:201:SER:HB3	63:Sg:206:LEU:HB2	1.98	0.46
64:SA:10:MET:HE1	64:SA:18:PHE:CE2	2.51	0.46
68:SG:49:VAL:HB	68:SG:115:LYS:HG2	1.98	0.46
82:S2:455:A:H2'	82:S2:456:C:C6	2.51	0.46
82:S2:845:G:H2'	82:S2:846:G:C8	2.50	0.46
82:S2:1438:A:H2'	82:S2:1439:A:C8	2.50	0.46
2:L5:97:G:OP1	15:LL:16:LYS:NZ	2.43	0.45
2:L5:711:A:H2'	2:L5:712:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3680:U:OP1	5:LA:54:ARG:NH2	2.32	0.45
2:L5:4322:G:N2	2:L5:4325:A:OP2	2.38	0.45
2:L5:4457:PSU:H1'	6:LB:252:ALA:HB3	1.98	0.45
6:LB:220:ILE:HB	6:LB:346:THR:HB	1.98	0.45
11:LG:166:LEU:HA	17:LN:7:ILE:HD11	1.98	0.45
19:LP:54:GLN:HA	19:LP:83:TRP:CD1	2.51	0.45
28:LY:74:TYR:HD1	28:LY:77:LYS:H	1.64	0.45
31:Lb:65:MET:HG2	31:Lb:68:ARG:NH1	2.30	0.45
47:Ls:78:LEU:O	47:Ls:82:ILE:HG12	2.15	0.45
54:SQ:125:ARG:HB2	82:S2:1648:G:H5''	1.98	0.45
56:SS:121:ARG:NH1	82:S2:1611:G:OP2	2.49	0.45
68:SG:87:ARG:HD3	68:SG:87:ARG:HA	1.71	0.45
69:SH:162:GLN:HE22	69:SH:166:VAL:HB	1.81	0.45
80:Sb:8:LEU:HD23	80:Sb:9:HIS:ND1	2.30	0.45
2:L5:2351:OMC:HM23	2:L5:2351:OMC:H1'	1.79	0.45
2:L5:4153:C:H2'	2:L5:4154:G:C8	2.52	0.45
4:L8:111:U:P	41:Ll:8:ARG:HE	2.40	0.45
6:LB:258:HIS:HA	6:LB:260:ALA:N	2.30	0.45
8:LD:51:MET:HE1	8:LD:163:LEU:HA	1.97	0.45
26:LW:7:SER:OG	26:LW:8:PHE:N	2.49	0.45
54:SQ:90:LYS:HB3	54:SQ:90:LYS:HE2	1.84	0.45
70:SI:101:ILE:HD11	70:SI:202:ILE:HD11	1.98	0.45
72:SL:22:ARG:NH1	72:SL:23:VAL:O	2.49	0.45
82:S2:27:A2M:HM'3	82:S2:27:A2M:H1'	1.65	0.45
82:S2:1232:PSU:H2'	82:S2:1233:G:C8	2.51	0.45
82:S2:1856:C:H2'	82:S2:1857:G:C8	2.51	0.45
2:L5:272:U:H2'	2:L5:273:U:C6	2.52	0.45
2:L5:1982:G:N2	2:L5:2009:A:HO2'	2.14	0.45
2:L5:4591:U:H2'	2:L5:4592:C:C6	2.51	0.45
6:LB:50:LYS:HB2	6:LB:345:LEU:HD11	1.97	0.45
7:LC:110:ARG:O	7:LC:113:ARG:NH1	2.44	0.45
21:LR:139:MET:HG2	21:LR:143:HIS:CE1	2.51	0.45
36:Lg:41:ALA:O	36:Lg:52:ARG:HD3	2.15	0.45
37:Lh:89:ARG:O	37:Lh:93:ARG:HG2	2.17	0.45
49:SD:108:LYS:HE3	49:SD:113:LEU:HD22	1.99	0.45
50:SF:192:LYS:HD3	50:SF:195:GLU:OE2	2.15	0.45
51:SK:37:ASP:OD1	51:SK:37:ASP:N	2.49	0.45
53:SP:18:ARG:NE	56:SS:88:LYS:HG2	2.31	0.45
65:SB:57:ILE:HG22	65:SB:59:SER:H	1.81	0.45
71:SJ:150:ARG:HG3	82:S2:821:G:C6	2.51	0.45
82:S2:575:A:H2'	82:S2:576:A2M:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:600:G:H2'	82:S2:601:OMG:H8	1.80	0.45
82:S2:1408:U:H2'	82:S2:1409:A:C8	2.52	0.45
82:S2:1457:U:H2'	82:S2:1458:G:C8	2.52	0.45
2:L5:1802:A:H5''	2:L5:1803:G:H5'	1.98	0.45
2:L5:1977:C:O2'	2:L5:1978:C:OP1	2.32	0.45
2:L5:3923:A:H2'	2:L5:3924:C:C6	2.52	0.45
2:L5:4184:G:H5'	5:LA:233:ARG:HB2	1.98	0.45
3:L7:26:C:O2'	14:LJ:147:ARG:NH1	2.49	0.45
8:LD:179:ARG:HD3	8:LD:179:ARG:HA	1.69	0.45
31:Lb:5:LYS:HE2	31:Lb:8:THR:HB	1.97	0.45
51:SK:23:ALA:HB3	51:SK:69:TRP:HH2	1.82	0.45
69:SH:25:GLN:HE22	69:SH:28:LEU:HD23	1.81	0.45
73:SN:26:LEU:HD21	73:SN:60:VAL:HG12	1.99	0.45
82:S2:348:A:H2'	82:S2:349:A:C8	2.51	0.45
82:S2:674:C:H2'	82:S2:675:U:C6	2.51	0.45
82:S2:1128:C:H2'	82:S2:1129:G:C8	2.51	0.45
82:S2:1560:U:O2'	82:S2:1583:C:O2'	2.27	0.45
83:Zt:4:C:H2'	83:Zt:5:G:C8	2.51	0.45
2:L5:1199:G:H2'	2:L5:1200:G:C8	2.52	0.45
2:L5:1359:G:H4'	17:LN:203:TYR:HB2	1.98	0.45
2:L5:2034:G:H2'	2:L5:2035:C:C6	2.51	0.45
2:L5:2093:A:N3	2:L5:2094:G:N1	2.65	0.45
2:L5:2656:U:OP1	29:LZ:78:ASN:ND2	2.50	0.45
2:L5:2759:G:O2'	2:L5:2760:G:O4'	2.32	0.45
8:LD:122:GLN:HG2	8:LD:124:GLU:O	2.17	0.45
24:LU:99:TRP:CH2	84:CI:59:GLN:CA	2.95	0.45
28:LY:2:LYS:HD2	28:LY:7:VAL:HG23	1.99	0.45
55:SR:111:PHE:CE2	64:SA:15:VAL:HG21	2.52	0.45
64:SA:184:ARG:HG3	64:SA:189:ILE:HD12	1.99	0.45
65:SB:63:LYS:HE3	65:SB:90:ASP:HA	1.99	0.45
68:SG:52:ILE:HG23	68:SG:109:LEU:HD11	1.99	0.45
82:S2:508:A:H3'	82:S2:509:OMG:C8	2.50	0.45
82:S2:649:PSU:H2'	82:S2:650:A:C8	2.51	0.45
82:S2:907:G:H2'	82:S2:908:A:C8	2.51	0.45
82:S2:1736:G:H2'	82:S2:1737:G:H8	1.82	0.45
82:S2:1807:C:H2'	82:S2:1808:U:C6	2.51	0.45
2:L5:24:G:N7	39:Lj:46:LYS:NZ	2.64	0.45
2:L5:1890:G:OP2	2:L5:1890:G:N2	2.46	0.45
2:L5:2558:C:H2'	2:L5:2559:G:H8	1.82	0.45
8:LD:55:VAL:HG22	8:LD:60:ILE:HD12	1.99	0.45
9:LE:119:GLU:HG3	34:Le:7:LEU:HD22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LO:153:THR:O	18:LO:157:GLU:HG2	2.17	0.45
24:LU:28:PRO:O	24:LU:32:GLY:N	2.49	0.45
49:SD:1:MET:SD	49:SD:2:ALA:N	2.90	0.45
53:SP:56:LEU:HD13	53:SP:80:LEU:HD11	1.97	0.45
53:SP:108:LYS:H	53:SP:111:MET:CE	2.29	0.45
63:Sg:240:CYS:HG	63:Sg:291:TRP:CD1	2.35	0.45
65:SB:160:GLN:O	65:SB:164:ILE:HG12	2.16	0.45
80:Sb:36:LYS:NZ	80:Sb:80:ARG:HE	2.15	0.45
82:S2:454:U:H2'	82:S2:455:A:C8	2.52	0.45
82:S2:494:C:N4	82:S2:509:OMG:HN22	2.14	0.45
83:Zt:4:C:H2'	83:Zt:5:G:H8	1.82	0.45
2:L5:909:A:H2'	2:L5:910:G:H8	1.82	0.45
2:L5:1403:G:N2	2:L5:1415:G:C4	2.85	0.45
2:L5:1405:C:N3	2:L5:1413:C:N4	2.65	0.45
2:L5:2624:G:OP2	24:LU:97:ARG:NH2	2.49	0.45
2:L5:3856:A:H5''	19:LP:83:TRP:O	2.17	0.45
2:L5:3932:U:H2'	2:L5:3933:G:C8	2.51	0.45
2:L5:4420:U:H5''	2:L5:4421:C:C5	2.50	0.45
6:LB:46:PHE:CE2	6:LB:81:THR:HB	2.50	0.45
53:SP:120:SER:OG	53:SP:120:SER:O	2.32	0.45
59:SZ:62:VAL:HA	59:SZ:65:TYR:HE1	1.81	0.45
64:SA:111:GLN:HA	64:SA:116:PHE:CG	2.51	0.45
65:SB:32:ASP:O	65:SB:96:CYS:N	2.44	0.45
70:SI:139:LYS:HE2	70:SI:139:LYS:HB2	1.63	0.45
82:S2:433:A:H2'	82:S2:434:G:C8	2.52	0.45
82:S2:626:G:N2	82:S2:626:G:OP2	2.50	0.45
2:L5:162:A:H2'	2:L5:163:A:C8	2.52	0.45
2:L5:351:C:OP2	7:LC:197:ARG:NH1	2.33	0.45
2:L5:748:G:O6	22:LS:98:ARG:NH2	2.50	0.45
2:L5:2394:G:O2'	2:L5:2819:U:O4	2.26	0.45
2:L5:3656:A:HO2'	2:L5:3747:A:HO2'	1.62	0.45
2:L5:3830:A2M:HM'3	2:L5:3830:A2M:H1'	1.72	0.45
2:L5:3841:OMC:HM23	2:L5:3841:OMC:H1'	1.83	0.45
2:L5:4401:G:H2'	2:L5:4402:C:H6	1.81	0.45
2:L5:4571:A2M:H2'	2:L5:4572:U:C6	2.52	0.45
6:LB:184:GLN:HG2	6:LB:186:ASN:HD21	1.81	0.45
12:LH:102:ASN:HB2	12:LH:115:ARG:HB2	1.98	0.45
18:LO:168:TYR:CE2	18:LO:172:LYS:HD2	2.52	0.45
21:LR:127:VAL:HG12	21:LR:132:PHE:HD2	1.81	0.45
28:LY:30:MET:HB3	28:LY:101:PRO:HG3	1.98	0.45
34:Le:35:TRP:CZ2	34:Le:56:PRO:HD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SP:47:ARG:HE	82:S2:1619:A:P	2.39	0.45
56:SS:40:TYR:HD1	56:SS:83:PHE:HE2	1.65	0.45
76:SW:22:LYS:NZ	82:S2:1096:G:OP1	2.49	0.45
80:Sb:33:MET:HE3	80:Sb:48:SER:HA	1.98	0.45
82:S2:461:U:H2'	82:S2:462:OMC:C6	2.52	0.45
82:S2:749:U:H3	82:S2:793:G:N2	2.15	0.45
82:S2:884:C:H2'	82:S2:885:U:O4'	2.17	0.45
82:S2:1550:G:O2'	82:S2:1558:C:O2	2.28	0.45
1:Pt:27:U:H2'	1:Pt:28:U:H6	1.82	0.45
2:L5:1320:U:O2'	2:L5:1891:A:N1	2.48	0.45
2:L5:4304:A:OP2	2:L5:4305:G:N2	2.49	0.45
4:L8:41:A:H4'	39:Lj:59:THR:HG23	1.99	0.45
6:LB:165:HIS:ND1	6:LB:166:THR:O	2.47	0.45
29:LZ:81:MET:HE1	32:Lc:59:GLU:HG3	1.99	0.45
34:Le:91:CYS:HB3	34:Le:95:TYR:CD2	2.51	0.45
38:Li:81:ILE:HD12	38:Li:84:LYS:HE2	1.99	0.45
52:SM:33:ARG:NH2	82:S2:1313:A:OP2	2.48	0.45
63:Sg:124:SER:OG	63:Sg:125:ARG:N	2.50	0.45
63:Sg:215:GLN:HA	63:Sg:231:ASP:HA	1.98	0.45
64:SA:42:LYS:HG3	64:SA:46:ILE:HB	1.99	0.45
68:SG:41:LEU:HD23	68:SG:41:LEU:H	1.82	0.45
70:SI:98:LYS:HG3	70:SI:178:ARG:HG2	1.99	0.45
78:SY:99:LYS:HA	78:SY:101:LYS:NZ	2.32	0.45
80:Sb:81:ARG:HA	80:Sb:81:ARG:HD3	1.82	0.45
82:S2:16:G:H2'	82:S2:17:C:C6	2.51	0.45
82:S2:160:U:C4	82:S2:468:A2M:H4'	2.52	0.45
82:S2:224:A:H2'	82:S2:225:G:C8	2.52	0.45
82:S2:693:A:H2'	82:S2:694:G:C8	2.52	0.45
82:S2:1174:PSU:H2'	82:S2:1175:G:H8	1.82	0.45
2:L5:458:C:H2'	2:L5:459:C:H6	1.81	0.45
2:L5:729:G:O6	22:LS:68:PHE:N	2.44	0.45
2:L5:1565:A:C5	2:L5:1566:C:H1'	2.51	0.45
2:L5:3718:A2M:H2'	2:L5:3719:A:O4'	2.17	0.45
2:L5:4636:PSU:N1	33:Ld:79:ASN:OD1	2.50	0.45
2:L5:5053:U:H5'	2:L5:5054:C:C5	2.52	0.45
4:L8:120:G:H2'	4:L8:121:G:H8	1.82	0.45
21:LR:138:LEU:O	21:LR:142:ILE:HG13	2.17	0.45
25:LV:107:ASN:OD1	25:LV:111:GLU:N	2.49	0.45
30:La:63:LEU:HD22	30:La:65:ARG:NH1	2.32	0.45
47:Ls:58:ASN:HA	47:Ls:61:MET:HE2	1.99	0.45
53:SP:125:PRO:HG3	56:SS:127:TRP:CH2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Sg:213:ASP:OD1	63:Sg:213:ASP:N	2.48	0.45
69:SH:8:ILE:HD11	69:SH:28:LEU:HD13	1.99	0.45
70:SI:105:ASP:OD1	70:SI:107:THR:HG23	2.17	0.45
77:SX:17:ARG:HH12	82:S2:659:G:H21	1.64	0.45
80:Sb:34:ASP:OD1	80:Sb:80:ARG:HG2	2.17	0.45
82:S2:1579:A:H4'	82:S2:1581:C:H5	1.82	0.45
82:S2:1705:C:H2'	82:S2:1706:G:C8	2.52	0.45
2:L5:501:C:O2'	2:L5:648:G:OP1	2.26	0.44
2:L5:705:G:H2'	2:L5:706:C:C6	2.52	0.44
2:L5:1514:U:H2'	2:L5:1515:A:C8	2.52	0.44
2:L5:1591:U:OP2	2:L5:2856:C:O2'	2.28	0.44
2:L5:1979:A:N6	2:L5:1984:A:OP1	2.51	0.44
2:L5:2539:C:H2'	2:L5:2540:C:C6	2.52	0.44
2:L5:2845:A:H61	2:L5:3843:C:N4	2.10	0.44
2:L5:3893:C:H2'	2:L5:3894:A:C8	2.52	0.44
2:L5:4957:C:H2'	2:L5:4958:C:C6	2.53	0.44
9:LE:115:TYR:CD1	46:Lr:115:SER:HB3	2.51	0.44
18:LO:73:PHE:HB3	18:LO:78:ARG:HB3	1.98	0.44
57:ST:12:GLN:HE22	82:S2:1593:C:H1'	1.82	0.44
59:SZ:80:ARG:HE	82:S2:1598:G:P	2.40	0.44
64:SA:32:PHE:CG	82:S2:1097:G:H4'	2.52	0.44
68:SG:170:ARG:HA	82:S2:72:C:H42	1.82	0.44
77:SX:140:ARG:HE	77:SX:141:PRO:HD2	1.82	0.44
82:S2:388:U:H2'	82:S2:389:A:H8	1.81	0.44
82:S2:1337:4AC:H2'	82:S2:1338:G:H8	1.82	0.44
82:S2:1643:U:H2'	82:S2:1644:C:C6	2.51	0.44
82:S2:1716:C:H2'	82:S2:1717:C:H6	1.81	0.44
2:L5:662:C:H2'	2:L5:663:G:C8	2.53	0.44
2:L5:959:G:O2'	2:L5:2263:A:N6	2.50	0.44
2:L5:1340:OMC:H1'	2:L5:1340:OMC:HM23	1.69	0.44
2:L5:1556:C:O2'	2:L5:2669:C:OP1	2.28	0.44
2:L5:2073:C:OP1	10:LF:212:LYS:HE3	2.17	0.44
2:L5:2676:A:OP2	2:L5:2676:A:H8	2.00	0.44
2:L5:2875:C:OP1	45:Lp:23:ARG:NH2	2.50	0.44
2:L5:3656:A:H2'	2:L5:3657:U:H6	1.82	0.44
2:L5:3867:A2M:HM'3	2:L5:3867:A2M:H1'	1.59	0.44
2:L5:4494:OMG:OP1	25:LV:49:LEU:HD12	2.17	0.44
2:L5:4926:C:H5''	2:L5:4927:G:H21	1.82	0.44
3:L7:63:C:H5'	3:L7:64:G:H5''	1.99	0.44
4:L8:21:C:OP1	7:LC:195:LYS:NZ	2.48	0.44
8:LD:203:ASN:OD1	8:LD:203:ASN:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LH:49:GLY:O	12:LH:53:LYS:NZ	2.45	0.44
16:LM:24:LEU:HB2	16:LM:43:THR:HG21	1.99	0.44
21:LR:103:ARG:HG2	21:LR:124:TYR:CE2	2.52	0.44
52:SM:112:LYS:HE2	52:SM:112:LYS:HB2	1.72	0.44
54:SQ:46:THR:HB	54:SQ:47:LEU:HD12	1.99	0.44
55:SR:7:LYS:HG3	82:S2:1373:C:OP1	2.17	0.44
56:SS:129:LEU:HA	56:SS:144:ARG:HH21	1.81	0.44
64:SA:219:GLU:HA	64:SA:222:VAL:HG12	1.98	0.44
82:S2:484:A2M:H8	82:S2:484:A2M:O5'	2.16	0.44
82:S2:641:A:H2'	82:S2:642:U:O4'	2.18	0.44
82:S2:668:A2M:H2'	82:S2:669:A:N7	2.32	0.44
83:Zt:37:A:H3'	83:Zt:38:A:H8	1.81	0.44
2:L5:162:A:H2'	2:L5:163:A:H8	1.82	0.44
2:L5:184:U:H3	2:L5:253:G:H1	1.65	0.44
2:L5:1176:C:H42	2:L5:1184:A:H61	1.64	0.44
2:L5:1294:A:H1'	2:L5:1296:G:N1	2.32	0.44
2:L5:1504:G:H2'	2:L5:1505:C:C6	2.52	0.44
2:L5:2666:U:OP2	21:LR:124:TYR:OH	2.22	0.44
2:L5:2739:C:O2	5:LA:188:LYS:NZ	2.51	0.44
2:L5:3848:U:H2'	2:L5:3849:A:H8	1.82	0.44
2:L5:4619:U:H2'	2:L5:4620:OMU:H6	1.98	0.44
4:L8:75:OMG:HM23	4:L8:75:OMG:H1'	1.79	0.44
6:LB:77:THR:OG1	6:LB:335:GLY:O	2.30	0.44
8:LD:129:GLU:OE2	8:LD:175:HIS:NE2	2.51	0.44
11:LG:177:MET:HE2	38:Li:39:PHE:CZ	2.51	0.44
14:LJ:56:THR:HG23	14:LJ:63:ARG:HA	1.99	0.44
16:LM:96:GLU:OE2	16:LM:100:ARG:NH2	2.43	0.44
18:LO:124:LEU:HB3	18:LO:126:VAL:HG12	1.98	0.44
25:LV:87:SER:OG	26:LW:19:ARG:NH1	2.48	0.44
27:LX:124:VAL:HG22	27:LX:138:VAL:HG22	1.99	0.44
31:Lb:102:PRO:O	31:Lb:109:ARG:NH2	2.51	0.44
35:Lf:8:LYS:HB3	35:Lf:100:ARG:CZ	2.46	0.44
48:Lt:85:LEU:HD22	48:Lt:109:ILE:HD12	1.98	0.44
60:Sc:60:GLU:OE1	60:Sc:63:ARG:HG3	2.18	0.44
64:SA:126:ASP:HB3	64:SA:129:ALA:HB3	1.99	0.44
69:SH:160:LYS:HD2	69:SH:163:GLN:HE21	1.83	0.44
71:SJ:150:ARG:HG3	82:S2:821:G:O6	2.17	0.44
82:S2:804:U:H2'	82:S2:805:U:C6	2.53	0.44
82:S2:976:G:H2'	82:S2:977:C:C6	2.53	0.44
82:S2:1490:OMG:HM23	82:S2:1490:OMG:H1'	1.78	0.44
2:L5:1172:C:H42	2:L5:1188:C:H42	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2520:C:H2'	2:L5:2521:G:H8	1.81	0.44
2:L5:4975:G:O2'	2:L5:4977:A:N6	2.44	0.44
6:LB:258:HIS:HA	6:LB:260:ALA:H	1.82	0.44
48:Lt:19:GLY:HA3	48:Lt:59:THR:HG22	2.00	0.44
49:SD:13:ALA:HA	49:SD:16:ILE:HG22	2.00	0.44
52:SM:51:VAL:HG12	52:SM:77:ILE:HB	1.99	0.44
55:SR:29:HIS:HB2	63:Sg:36:ARG:NH2	2.32	0.44
55:SR:79:GLU:O	55:SR:83:ASN:HB2	2.16	0.44
56:SS:30:ILE:O	56:SS:33:ILE:HG22	2.17	0.44
66:SC:64:THR:HG22	66:SC:66:LEU:N	2.32	0.44
74:SO:61:LYS:NZ	74:SO:76:LEU:HB3	2.33	0.44
82:S2:654:A:OP2	82:S2:655:A:O2'	2.29	0.44
2:L5:1279:A:OP1	9:LE:131:LYS:NZ	2.43	0.44
2:L5:1942:A:N3	2:L5:4432:C:O2'	2.45	0.44
2:L5:2016:C:H2'	2:L5:2017:A:H8	1.83	0.44
2:L5:4092:G:H2'	2:L5:4093:G:O4'	2.17	0.44
2:L5:4883:C:H2'	2:L5:4884:G:C8	2.53	0.44
4:L8:60:G:P	27:LX:68:ARG:HH22	2.39	0.44
26:LW:103:ALA:O	26:LW:106:GLU:HG3	2.18	0.44
45:Lp:85:ARG:NH2	82:S2:938:A:O2'	2.51	0.44
52:SM:67:ALA:O	52:SM:71:GLU:HG3	2.18	0.44
55:SR:99:ASP:OD2	55:SR:101:ASP:HB2	2.18	0.44
58:SU:20:ILE:HA	58:SU:116:ILE:HA	1.99	0.44
69:SH:157:HIS:HB3	69:SH:190:PRO:HG3	1.99	0.44
71:SJ:174:LYS:HB2	82:S2:560:A:H5'	1.99	0.44
72:SL:111:VAL:HG11	72:SL:128:VAL:HG11	1.99	0.44
82:S2:328:U:O2'	82:S2:329:G:O5'	2.32	0.44
82:S2:420:G:O2'	82:S2:660:C:N3	2.44	0.44
82:S2:509:OMG:HM23	82:S2:509:OMG:H1'	1.79	0.44
2:L5:424:U:H2'	2:L5:425:U:C6	2.53	0.44
2:L5:1833:G:N2	2:L5:1835:G:O4'	2.50	0.44
2:L5:2415:U:H2'	2:L5:2416:G:C8	2.53	0.44
2:L5:4527:G:OP2	2:L5:4527:G:N2	2.48	0.44
2:L5:4881:U:C4	16:LM:113:MET:HG3	2.53	0.44
2:L5:4996:C:OP1	33:Ld:32:ARG:NH1	2.48	0.44
8:LD:223:PHE:HB3	8:LD:226:TYR:HB2	1.98	0.44
23:LT:44:GLY:HA2	23:LT:95:HIS:HB3	1.98	0.44
37:Lh:70:ARG:HG2	37:Lh:83:LEU:HD22	1.98	0.44
51:SK:60:GLU:HG2	51:SK:68:TYR:H	1.82	0.44
57:ST:62:ARG:CZ	82:S2:1542:C:H5''	2.48	0.44
78:SY:129:LYS:HA	78:SY:129:LYS:HD3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:388:U:H2'	82:S2:389:A:C8	2.53	0.44
82:S2:527:C:H2'	82:S2:528:A:C8	2.53	0.44
82:S2:1201:U:O2'	82:S2:1358:U:O2'	2.34	0.44
82:S2:1273:C:O2'	82:S2:1506:A:N1	2.38	0.44
2:L5:300:A:H2'	2:L5:301:G:H8	1.82	0.44
2:L5:1299:G:H2'	2:L5:1300:G:C8	2.52	0.44
2:L5:1631:A:C2	5:LA:204:MET:HG2	2.53	0.44
2:L5:1850:A:N3	2:L5:2283:G:O2'	2.50	0.44
2:L5:2468:U:O2'	2:L5:2506:G:N2	2.50	0.44
2:L5:2756:G:H2'	2:L5:2757:A:C8	2.53	0.44
2:L5:4278:C:H5'	23:LT:47:THR:HG23	2.00	0.44
2:L5:4580:U:O2'	6:LB:182:GLU:OE2	2.27	0.44
2:L5:4769:G:OP1	18:LO:176:ARG:NH1	2.38	0.44
3:L7:110:G:H2'	3:L7:111:C:C6	2.53	0.44
6:LB:161:ARG:HG2	6:LB:184:GLN:HA	2.00	0.44
7:LC:290:SER:O	7:LC:294:LYS:HG2	2.17	0.44
16:LM:11:ARG:HB3	16:LM:27:ILE:HD12	2.00	0.44
26:LW:56:ARG:HE	26:LW:61:LYS:HB2	1.82	0.44
28:LY:106:ILE:HG21	28:LY:109:LEU:HD23	1.99	0.44
32:Lc:78:ASN:OD1	32:Lc:78:ASN:N	2.50	0.44
33:Ld:93:ASN:O	33:Ld:95:ASP:N	2.49	0.44
37:Lh:80:PRO:HD2	37:Lh:83:LEU:HD12	2.00	0.44
51:SK:25:LYS:HE3	51:SK:67:PHE:CE1	2.53	0.44
53:SP:22:LEU:HA	53:SP:25:LEU:HB3	1.99	0.44
55:SR:34:VAL:O	55:SR:38:ILE:HG12	2.17	0.44
56:SS:105:ASN:O	56:SS:108:ARG:N	2.51	0.44
65:SB:118:GLN:O	82:S2:988:C:O2'	2.35	0.44
68:SG:7:PHE:CD2	68:SG:10:THR:HG22	2.53	0.44
70:SI:181:GLN:NE2	82:S2:380:G:OP2	2.47	0.44
75:SV:62:MET:HE2	80:Sb:3:LEU:HD21	2.00	0.44
82:S2:28:U:H2'	82:S2:29:G:C8	2.50	0.44
82:S2:1083:A:N7	82:S2:1841:C:O2'	2.44	0.44
1:Pt:51:C:H2'	1:Pt:52:G:C8	2.53	0.44
2:L5:170:C:H42	2:L5:266:C:N4	2.15	0.44
2:L5:713:C:H2'	2:L5:714:G:C8	2.52	0.44
2:L5:1726:U:H5'	10:LF:135:ILE:HD11	2.00	0.44
2:L5:3792:OMG:HM23	2:L5:3792:OMG:H1'	1.79	0.44
5:LA:22:HIS:O	5:LA:24:LYS:NZ	2.50	0.44
6:LB:288:GLY:HA3	6:LB:330:PHE:CE1	2.52	0.44
14:LJ:114:ASP:HB3	56:SS:14:ARG:NE	2.33	0.44
26:LW:99:GLU:HG2	26:LW:102:LYS:HE3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LZ:123:LYS:O	29:LZ:124:THR:OG1	2.30	0.44
32:Lc:18:LEU:HA	32:Lc:21:VAL:HG12	1.99	0.44
43:Ln:16:LYS:O	43:Ln:20:MET:HG2	2.16	0.44
51:SK:90:VAL:HG11	51:SK:95:ARG:HE	1.82	0.44
57:ST:39:LEU:HA	57:ST:39:LEU:HD23	1.70	0.44
57:ST:110:LEU:HD23	57:ST:112:MET:HE3	1.99	0.44
63:Sg:21:ILE:HG21	63:Sg:299:PHE:HB2	2.00	0.44
64:SA:77:ILE:HG13	64:SA:99:ILE:HB	2.00	0.44
70:SI:22:HIS:HB3	82:S2:433:A:H5''	2.00	0.44
72:SL:49:GLU:OE1	72:SL:116:CYS:HA	2.18	0.44
73:SN:69:ASN:HB3	73:SN:74:ILE:HD11	1.99	0.44
77:SX:17:ARG:HH12	82:S2:659:G:N2	2.15	0.44
82:S2:15:U:H2'	82:S2:16:G:O4'	2.17	0.44
82:S2:160:U:O4	82:S2:468:A2M:H4'	2.17	0.44
82:S2:1010:G:H2'	82:S2:1011:A:C8	2.53	0.44
82:S2:1177:PSU:H2'	82:S2:1178:U:C6	2.53	0.44
82:S2:1215:C:O2'	82:S2:1645:C:OP2	2.28	0.44
82:S2:1328:OMG:HM23	82:S2:1328:OMG:H1'	1.72	0.44
82:S2:1588:A:N3	82:S2:1654:G:O2'	2.47	0.44
2:L5:107:G:OP2	15:LL:42:LYS:NZ	2.46	0.44
2:L5:1825:A:H2'	2:L5:1826:G:C8	2.53	0.44
2:L5:1916:G:N3	2:L5:2067:C:O2'	2.50	0.44
2:L5:1974:U:H4'	2:L5:1975:G:H3'	1.99	0.44
2:L5:2108:G:N1	2:L5:2109:G:O6	2.51	0.44
2:L5:3896:C:O2'	6:LB:268:ARG:NH2	2.46	0.44
2:L5:4306:OMU:HM23	2:L5:4306:OMU:H1'	1.77	0.44
8:LD:120:GLU:O	8:LD:248:ARG:NH1	2.50	0.44
13:LI:85:PHE:HE2	13:LI:87:MET:HE1	1.83	0.44
19:LP:15:CYS:SG	19:LP:150:LEU:HB2	2.58	0.44
20:LQ:59:PRO:HG3	20:LQ:143:ARG:HA	1.99	0.44
23:LT:4:THR:OG1	23:LT:9:ARG:HD3	2.18	0.44
48:Lt:32:ILE:HA	48:Lt:35:LEU:HD23	1.99	0.44
55:SR:28:PHE:HA	55:SR:55:THR:HG21	1.99	0.44
62:Sf:123:SER:HG	62:Sf:126:CYS:H	1.66	0.44
62:Sf:143:LYS:NZ	82:S2:1310:U:O3'	2.50	0.44
63:Sg:194:TYR:CE1	63:Sg:212:LYS:HB2	2.53	0.44
65:SB:103:MET:HG2	65:SB:188:LEU:HD13	2.00	0.44
67:SE:148:ARG:NH2	68:SG:205:GLU:OE1	2.51	0.44
68:SG:135:PRO:HA	82:S2:169:U:H5''	1.99	0.44
82:S2:344:U:H2'	82:S2:345:U:C6	2.53	0.44
2:L5:264:C:H2'	2:L5:265:C:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1259:G:H2'	2:L5:1260:G:C8	2.53	0.43
2:L5:2351:OMC:HM22	7:LC:95:MET:HG3	1.98	0.43
2:L5:2611:A:H2'	2:L5:2612:G:C8	2.53	0.43
2:L5:4102:C:H1'	2:L5:4108:G:H1	1.83	0.43
4:L8:135:C:O3'	27:LX:56:ARG:NH1	2.51	0.43
10:LF:37:PHE:HZ	31:Lb:113:ALA:HB1	1.83	0.43
14:LJ:114:ASP:HB3	56:SS:14:ARG:HE	1.82	0.43
24:LU:22:THR:HA	24:LU:71:THR:HA	1.99	0.43
34:Le:91:CYS:HB3	34:Le:95:TYR:HD2	1.82	0.43
37:Lh:12:LYS:HZ2	37:Lh:12:LYS:HG2	1.60	0.43
42:Lm:99:CYS:HB2	42:Lm:114:LYS:HE3	1.99	0.43
62:Sf:123:SER:OG	62:Sf:144:CYS:HB3	2.18	0.43
63:Sg:119:GLN:HG3	63:Sg:179:LEU:HD21	2.00	0.43
66:SC:125:LYS:NZ	82:S2:1356:G:O3'	2.45	0.43
67:SE:36:HIS:ND1	67:SE:85:GLY:HA3	2.33	0.43
74:SO:30:VAL:HG23	74:SO:47:LEU:HA	2.00	0.43
77:SX:107:ARG:HG2	77:SX:112:VAL:HG22	1.99	0.43
82:S2:811:A:H2'	82:S2:812:A:C8	2.52	0.43
82:S2:991:G:C6	82:S2:1134:G:H4'	2.52	0.43
82:S2:1289:U:O4	82:S2:1311:C:N4	2.51	0.43
82:S2:1805:G:H2'	82:S2:1806:A:H8	1.84	0.43
2:L5:223:G:H4'	2:L5:225:G:C8	2.53	0.43
2:L5:260:C:H2'	2:L5:261:G:C8	2.54	0.43
2:L5:1194:G:H2'	2:L5:1195:G:C8	2.53	0.43
2:L5:2102:G:N2	2:L5:2104:G:H1	2.17	0.43
2:L5:2335:C:H2'	2:L5:2336:G:H8	1.83	0.43
2:L5:2340:C:H4'	7:LC:42:THR:HG23	1.99	0.43
10:LF:32:ARG:O	10:LF:36:LYS:HG2	2.18	0.43
12:LH:34:LEU:HD23	12:LH:34:LEU:HA	1.81	0.43
13:LI:51:HIS:CD2	13:LI:168:SER:HB2	2.53	0.43
16:LM:126:GLU:OE2	18:LO:181:ALA:HB1	2.18	0.43
40:Lk:16:ARG:HG2	40:Lk:61:PRO:HG3	1.99	0.43
44:Lo:74:GLU:HB3	44:Lo:77:CYS:HB3	2.00	0.43
50:SF:73:THR:O	50:SF:89:THR:HG21	2.17	0.43
54:SQ:96:TYR:HA	54:SQ:100:VAL:HG12	2.01	0.43
56:SS:36:VAL:HG22	56:SS:40:TYR:CD2	2.53	0.43
56:SS:125:HIS:HE1	82:S2:1609:C:H4'	1.83	0.43
63:Sg:270:LEU:HD13	63:Sg:310:TRP:CD2	2.52	0.43
67:SE:144:ALA:HB3	82:S2:121:OMU:HM23	1.99	0.43
71:SJ:109:ARG:NH2	71:SJ:111:GLN:OE1	2.46	0.43
74:SO:150:ARG:NH2	82:S2:1854:U:OP1	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SX:128:VAL:HG23	77:SX:138:LYS:HD2	2.00	0.43
80:Sb:68:GLY:C	82:S2:928:G:H21	2.26	0.43
82:S2:562:U:H2'	82:S2:563:G:C8	2.53	0.43
82:S2:601:OMG:HM23	82:S2:601:OMG:H1'	1.81	0.43
82:S2:1653:U:H3	82:S2:1671:G:H1	1.66	0.43
2:L5:309:C:H5''	2:L5:310:G:H5'	2.00	0.43
2:L5:736:C:OP1	16:LM:74:ARG:NH2	2.49	0.43
2:L5:1274:A:HO2'	2:L5:1275:G:H8	1.65	0.43
2:L5:1795:A:N3	3:L7:79:U:O2'	2.49	0.43
2:L5:1881:C:H5'	2:L5:2281:U:H1'	1.99	0.43
2:L5:1960:A:N3	47:Ls:14:PHE:HE2	2.16	0.43
2:L5:2424:OMG:H1'	2:L5:2424:OMG:HM23	1.83	0.43
2:L5:2884:G:H2'	2:L5:2885:A:H8	1.84	0.43
2:L5:3744:OMG:HM23	2:L5:3744:OMG:H1'	1.80	0.43
2:L5:4130:C:H2'	2:L5:4131:G:C8	2.53	0.43
6:LB:152:SER:O	6:LB:156:TYR:HB2	2.17	0.43
9:LE:207:LYS:O	9:LE:256:GLN:NE2	2.50	0.43
26:LW:96:GLN:HB3	26:LW:100:VAL:HB	2.00	0.43
37:Lh:8:ASP:OD1	37:Lh:8:ASP:N	2.51	0.43
44:Lo:30:LYS:HE2	44:Lo:30:LYS:HA	1.99	0.43
47:Ls:15:LEU:HA	47:Ls:18:ILE:HG22	2.00	0.43
52:SM:58:GLU:OE1	52:SM:61:TYR:N	2.51	0.43
54:SQ:137:ALA:N	82:S2:1650:A:OP1	2.50	0.43
56:SS:4:VAL:HB	59:SZ:51:ASP:HA	2.01	0.43
56:SS:63:GLU:O	56:SS:67:VAL:HG23	2.18	0.43
56:SS:86:ARG:HG3	56:SS:89:ASP:OD1	2.18	0.43
63:Sg:129:ILE:HD11	63:Sg:151:VAL:HG11	1.99	0.43
63:Sg:208:ALA:HB2	63:Sg:218:LEU:HD13	1.99	0.43
69:SH:70:LYS:HA	69:SH:73:GLN:HG3	2.00	0.43
70:SI:69:SER:OG	70:SI:70:GLU:OE1	2.29	0.43
70:SI:193:LYS:HA	70:SI:196:GLU:OE1	2.18	0.43
73:SN:70:LYS:O	73:SN:74:ILE:HG12	2.18	0.43
76:SW:77:PRO:HG2	76:SW:79:PHE:CE2	2.53	0.43
82:S2:1017:U:H2'	82:S2:1018:U:H6	1.83	0.43
82:S2:1644:C:H2'	82:S2:1645:C:C6	2.53	0.43
1:Pt:3:C:H2'	1:Pt:4:U:C6	2.54	0.43
1:Pt:71:A:H2'	1:Pt:72:C:C6	2.54	0.43
2:L5:170:C:H42	2:L5:266:C:H42	1.65	0.43
2:L5:473:C:H2'	2:L5:474:C:C6	2.53	0.43
2:L5:716:C:OP1	7:LC:317:ASN:HB2	2.18	0.43
2:L5:1080:C:C2	2:L5:1220:G:N2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2365:OMC:HM23	2:L5:2365:OMC:H1'	1.78	0.43
2:L5:2568:C:H2'	2:L5:2569:G:C8	2.53	0.43
2:L5:2844:A:N6	2:L5:3839:G:O2'	2.50	0.43
2:L5:2867:C:OP1	82:S2:368:U:N3	2.52	0.43
4:L8:39:G:H1'	4:L8:103:A:N6	2.34	0.43
11:LG:38:ASN:ND2	11:LG:43:GLN:OE1	2.51	0.43
12:LH:26:ILE:HG13	12:LH:35:ARG:HG3	2.00	0.43
29:LZ:136:PHE:O	36:Lg:78:TYR:OH	2.33	0.43
35:Lf:5:LEU:HA	35:Lf:5:LEU:HD23	1.85	0.43
47:Ls:141:LEU:HD23	47:Ls:143:ILE:HD11	2.00	0.43
49:SD:23:GLU:OE2	49:SD:27:ARG:NE	2.48	0.43
61:Sd:41:GLN:OE1	61:Sd:41:GLN:N	2.50	0.43
65:SB:129:THR:OG1	65:SB:131:ASP:OD1	2.34	0.43
66:SC:108:LYS:HB2	66:SC:233:LEU:HD23	2.01	0.43
71:SJ:86:VAL:HG11	71:SJ:105:PHE:CD1	2.53	0.43
72:SL:135:SER:O	72:SL:139:ARG:NH1	2.51	0.43
82:S2:59:U:O2'	82:S2:61:A:N7	2.48	0.43
82:S2:508:A:H5'	82:S2:509:OMG:OP2	2.19	0.43
82:S2:747:U:O2	82:S2:796:G:C2	2.70	0.43
82:S2:811:A:H2'	82:S2:812:A:H8	1.84	0.43
1:Pt:43:A:H2'	1:Pt:44:A:C8	2.54	0.43
2:L5:497:G:H21	2:L5:498:C:H5	1.66	0.43
2:L5:1404:G:N7	2:L5:1408:G:N1	2.66	0.43
2:L5:2380:G:N2	2:L5:2425:U:OP1	2.48	0.43
2:L5:3664:G:H2'	2:L5:3665:G:C8	2.54	0.43
2:L5:3708:C:H2'	2:L5:3709:U:C6	2.54	0.43
2:L5:3873:G:H2'	2:L5:3874:G:C8	2.54	0.43
2:L5:3925:OMU:HM23	2:L5:3925:OMU:H1'	1.66	0.43
2:L5:4392:OMG:HM21	2:L5:4394:A:H2'	2.00	0.43
2:L5:4970:C:C2	2:L5:4971:A:C8	3.06	0.43
7:LC:150:LEU:O	7:LC:152:LEU:N	2.51	0.43
10:LF:241:ASN:O	10:LF:245:ARG:HG2	2.19	0.43
16:LM:25:VAL:HB	16:LM:38:VAL:HG13	2.00	0.43
24:LU:99:TRP:CH2	84:CI:59:GLN:CB	2.98	0.43
47:Ls:41:GLN:O	47:Ls:45:MET:HG2	2.17	0.43
49:SD:215:ASP:N	49:SD:215:ASP:OD1	2.51	0.43
51:SK:49:MET:HE2	51:SK:69:TRP:CD2	2.54	0.43
53:SP:61:ARG:NH2	53:SP:88:GLU:OE2	2.51	0.43
58:SU:28:ASN:OD1	58:SU:29:VAL:N	2.51	0.43
65:SB:108:ASP:OD2	79:Sa:66:LYS:N	2.50	0.43
67:SE:242:LYS:HD3	67:SE:242:LYS:HA	1.73	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SH:142:LYS:HB3	76:SW:54:ASP:HB3	2.01	0.43
70:SI:126:GLY:O	70:SI:128:LYS:NZ	2.48	0.43
77:SX:22:TRP:HE3	77:SX:28:LYS:HD2	1.83	0.43
82:S2:468:A2M:H1'	82:S2:468:A2M:HM'3	1.65	0.43
82:S2:511:U:H2'	82:S2:512:A:C8	2.53	0.43
82:S2:548:C:H2'	82:S2:549:C:C6	2.53	0.43
2:L5:10:A:H2'	2:L5:11:G:H8	1.83	0.43
2:L5:186:G:H4'	2:L5:187:U:O4'	2.18	0.43
2:L5:1180:C:O2	2:L5:1183:C:N4	2.52	0.43
2:L5:1557:C:H2'	2:L5:1558:A:C8	2.54	0.43
2:L5:1662:C:H2'	2:L5:1663:C:C6	2.53	0.43
2:L5:1834:U:C2	23:LT:128:LEU:HD12	2.53	0.43
2:L5:2279:A:O2'	34:Le:48:ARG:NH2	2.51	0.43
2:L5:2458:C:O2'	2:L5:3671:G:N3	2.41	0.43
2:L5:3937:C:O2'	17:LN:124:ASP:OD1	2.37	0.43
8:LD:156:GLY:HA2	8:LD:181:PRO:HG3	2.01	0.43
11:LG:230:TYR:CE2	11:LG:234:ARG:HD2	2.54	0.43
14:LJ:81:GLU:O	14:LJ:84:GLU:HG3	2.18	0.43
14:LJ:87:LEU:O	14:LJ:91:GLU:N	2.52	0.43
14:LJ:119:TYR:CG	56:SS:12:ILE:HG22	2.53	0.43
15:LL:111:GLN:HA	15:LL:114:VAL:HG22	2.00	0.43
35:Lf:106:TYR:O	35:Lf:108:SER:N	2.51	0.43
36:Lg:60:ARG:HD2	36:Lg:60:ARG:HA	1.78	0.43
50:SF:70:GLU:OE2	50:SF:86:LYS:NZ	2.39	0.43
54:SQ:3:SER:OG	54:SQ:4:LYS:N	2.51	0.43
59:SZ:41:ARG:NH1	82:S2:1600:G:OP2	2.44	0.43
62:Sf:89:LYS:O	82:S2:1507:G:N2	2.40	0.43
63:Sg:66:VAL:HA	63:Sg:82:SER:HA	2.01	0.43
63:Sg:251:ALA:HB1	63:Sg:286:CYS:HB3	2.00	0.43
72:SL:111:VAL:HG12	72:SL:140:PHE:HB2	2.00	0.43
75:SV:65:SER:O	75:SV:68:SER:OG	2.33	0.43
78:SY:3:ASP:N	78:SY:3:ASP:OD1	2.50	0.43
82:S2:881:G:N2	82:S2:906:U:H1'	2.32	0.43
82:S2:1036:A:H4'	82:S2:1855:G:N2	2.34	0.43
82:S2:1174:PSU:H2'	82:S2:1175:G:C8	2.54	0.43
2:L5:737:C:OP2	16:LM:71:LYS:NZ	2.52	0.43
2:L5:1616:U:H2'	2:L5:1617:G:H8	1.84	0.43
2:L5:1725:U:H2'	2:L5:1726:U:C6	2.53	0.43
2:L5:1820:C:H5'	8:LD:139:PRO:HB3	2.01	0.43
2:L5:1997:U:H2'	2:L5:1998:A:H3'	2.01	0.43
3:L7:57:C:H2'	3:L7:58:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LB:74:GLU:OE1	6:LB:285:TYR:OH	2.34	0.43
6:LB:389:MET:HE2	6:LB:392:LEU:HD21	2.00	0.43
10:LF:83:VAL:HG21	23:LT:139:HIS:CE1	2.53	0.43
24:LU:99:TRP:CE3	84:CI:58:LEU:CG	3.01	0.43
26:LW:57:ARG:NH2	26:LW:61:LYS:O	2.52	0.43
27:LX:101:ASP:OD1	27:LX:102:VAL:N	2.51	0.43
28:LY:4:ASN:HB3	28:LY:7:VAL:HG22	1.99	0.43
34:Le:76:LYS:HE2	34:Le:98:GLU:OE2	2.19	0.43
43:Ln:17:ARG:NH1	82:S2:1173:A:OP1	2.52	0.43
46:Lr:39:ARG:NH1	46:Lr:105:ASP:OD2	2.51	0.43
52:SM:20:GLU:O	52:SM:23:LYS:HG3	2.18	0.43
56:SS:15:VAL:HG13	56:SS:68:ILE:HD11	2.00	0.43
58:SU:74:SER:H	82:S2:1338:G:H4'	1.84	0.43
63:Sg:209:SER:O	63:Sg:217:MET:N	2.50	0.43
65:SB:117:TRP:HB3	65:SB:153:THR:HA	2.01	0.43
67:SE:36:HIS:CG	67:SE:85:GLY:HA3	2.54	0.43
68:SG:13:GLN:HE21	82:S2:153:G:H21	1.66	0.43
68:SG:191:ARG:NH2	82:S2:312:G:H2'	2.32	0.43
76:SW:28:ARG:HD3	82:S2:921:G:C5	2.54	0.43
76:SW:79:PHE:N	76:SW:125:ILE:HG22	2.34	0.43
82:S2:386:C:H2'	82:S2:387:C:C6	2.53	0.43
82:S2:484:A2M:HM'3	82:S2:484:A2M:H1'	1.88	0.43
82:S2:1562:C:H2'	82:S2:1563:G:C8	2.54	0.43
83:Zt:51:G:H2'	83:Zt:52:G:H8	1.84	0.43
2:L5:267:G:H2'	2:L5:268:G:C8	2.54	0.43
2:L5:1705:G:H2'	2:L5:1706:A:C8	2.54	0.43
2:L5:1845:U:OP1	31:Lb:25:ARG:HG3	2.19	0.43
2:L5:4098:A:N1	2:L5:4112:C:N4	2.66	0.43
2:L5:4590:A2M:H1'	2:L5:4590:A2M:HM'3	1.62	0.43
2:L5:4723:A:H2'	2:L5:4724:A:C8	2.54	0.43
2:L5:4738:C:H2'	2:L5:4739:C:C6	2.54	0.43
2:L5:4860:G:H2'	2:L5:4861:G:H8	1.82	0.43
20:LQ:69:LYS:HA	20:LQ:69:LYS:HD3	1.87	0.43
20:LQ:154:LYS:HE2	20:LQ:154:LYS:HB3	1.74	0.43
30:La:75:LEU:HD23	30:La:75:LEU:HA	1.85	0.43
47:Ls:30:VAL:HG21	47:Ls:187:LEU:HG	2.00	0.43
47:Ls:82:ILE:HD12	47:Ls:88:PHE:HE1	1.83	0.43
61:Sd:3:HIS:CE1	61:Sd:5:GLN:HB3	2.54	0.43
61:Sd:21:CYS:SG	61:Sd:39:CYS:N	2.87	0.43
63:Sg:239:LEU:HG	63:Sg:248:LEU:HD11	2.01	0.43
71:SJ:136:ARG:HA	71:SJ:141:VAL:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:SY:119:GLY:O	82:S2:84:A:O2'	2.30	0.43
80:Sb:8:LEU:HD23	80:Sb:9:HIS:CE1	2.53	0.43
82:S2:98:C:OP2	82:S2:426:A:O2'	2.28	0.43
82:S2:518:G:H2'	82:S2:519:A:H8	1.84	0.43
82:S2:1539:U:H2'	82:S2:1540:G:C8	2.54	0.43
2:L5:7:C:H2'	2:L5:8:U:C6	2.54	0.43
2:L5:123:C:H2'	2:L5:124:C:H6	1.83	0.43
2:L5:257:C:H2'	2:L5:258:G:C8	2.54	0.43
2:L5:1081:C:O2'	2:L5:1082:C:H5'	2.18	0.43
2:L5:2092:G:O2'	2:L5:2093:A:OP2	2.35	0.43
2:L5:4589:A:N1	2:L5:4621:C:O2'	2.45	0.43
6:LB:140:GLU:O	6:LB:144:LYS:HG2	2.18	0.43
6:LB:196:TRP:CD1	6:LB:200:ARG:HH12	2.37	0.43
6:LB:394:LYS:HA	6:LB:397:ILE:HG12	2.00	0.43
7:LC:291:ARG:NH2	46:Lr:46:ARG:HH12	2.16	0.43
10:LF:182:TYR:HB3	10:LF:200:ARG:HG3	2.01	0.43
11:LG:102:TYR:OH	11:LG:211:ASP:OD2	2.34	0.43
14:LJ:55:TYR:HA	14:LJ:64:ARG:HG2	2.01	0.43
15:LL:18:TRP:CD1	15:LL:18:TRP:H	2.36	0.43
17:LN:200:LEU:HD22	17:LN:204:ARG:NH1	2.33	0.43
18:LO:6:VAL:HA	18:LO:32:LYS:HB2	2.01	0.43
32:Lc:35:LEU:O	32:Lc:39:ARG:HG2	2.18	0.43
35:Lf:46:ARG:HD3	35:Lf:72:GLY:O	2.18	0.43
36:Lg:33:LEU:HD23	36:Lg:33:LEU:HA	1.80	0.43
38:Li:68:ARG:HD3	38:Li:68:ARG:HA	1.82	0.43
50:SF:182:LYS:HE3	50:SF:182:LYS:HB2	1.84	0.43
51:SK:23:ALA:HB3	51:SK:69:TRP:CH2	2.54	0.43
57:ST:139:ALA:C	57:ST:143:LYS:HZ2	2.27	0.43
61:Sd:8:TRP:CZ3	82:S2:1512:C:H5''	2.54	0.43
65:SB:77:ASP:N	65:SB:78:GLU:OE1	2.51	0.43
66:SC:238:LYS:NZ	82:S2:1355:C:O2'	2.37	0.43
66:SC:256:TRP:CD2	76:SW:68:ARG:HD3	2.53	0.43
69:SH:76:GLN:OE1	69:SH:94:PHE:HB2	2.19	0.43
70:SI:88:ASN:O	70:SI:91:VAL:HG22	2.17	0.43
74:SO:28:PHE:HZ	79:Sa:58:VAL:HG21	1.84	0.43
75:SV:27:LYS:HD3	75:SV:27:LYS:HA	1.85	0.43
75:SV:58:ALA:HA	75:SV:61:ARG:HG2	2.00	0.43
79:Sa:13:LYS:HD3	79:Sa:13:LYS:HA	1.70	0.43
80:Sb:53:VAL:HG13	80:Sb:62:VAL:HG23	2.01	0.43
82:S2:29:G:H2'	82:S2:30:C:C6	2.54	0.43
82:S2:140:C:H2'	82:S2:141:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:293:C:O2'	82:S2:294:U:H3'	2.18	0.43
82:S2:1435:C:O2'	82:S2:1436:C:O4'	2.29	0.43
82:S2:1797:U:H2'	82:S2:1798:C:C6	2.53	0.43
83:Zt:62:C:H2'	83:Zt:63:C:C6	2.54	0.43
2:L5:138:G:H2'	2:L5:139:G:C8	2.54	0.43
2:L5:458:C:H2'	2:L5:459:C:C6	2.54	0.43
2:L5:654:C:H2'	2:L5:655:C:C6	2.54	0.43
2:L5:1941:A:C2	2:L5:4434:C:H5'	2.54	0.43
2:L5:4620:OMU:HM23	2:L5:4620:OMU:H1'	1.69	0.43
2:L5:5001:PSU:H2'	2:L5:5002:U:O4'	2.18	0.43
7:LC:5:ARG:HH21	7:LC:25:PRO:HA	1.84	0.43
8:LD:263:LYS:HD3	8:LD:263:LYS:HA	1.82	0.43
11:LG:83:PHE:HA	11:LG:183:ILE:HD13	2.01	0.43
17:LN:126:THR:HG23	17:LN:127:TYR:CD2	2.54	0.43
40:Lk:61:PRO:HA	40:Lk:62:PRO:HD3	1.92	0.43
44:Lo:30:LYS:CE	83:Zt:74:C:H5''	2.48	0.43
61:Sd:29:GLY:O	61:Sd:40:ARG:N	2.52	0.43
64:SA:90:PHE:CD1	64:SA:179:ALA:HB2	2.54	0.43
64:SA:184:ARG:HH21	64:SA:191:ARG:C	2.26	0.43
65:SB:24:PRO:HA	65:SB:27:LYS:NZ	2.34	0.43
82:S2:159:A2M:H1'	82:S2:159:A2M:HM'3	1.64	0.43
82:S2:455:A:H2'	82:S2:456:C:H6	1.84	0.43
82:S2:644:OMG:HM23	82:S2:644:OMG:H1'	1.69	0.43
82:S2:689:U:H2'	82:S2:690:G:C4	2.54	0.43
82:S2:1177:PSU:H2'	82:S2:1178:U:H6	1.83	0.43
82:S2:1680:G:H2'	82:S2:1681:U:C6	2.53	0.43
82:S2:1736:G:H2'	82:S2:1737:G:C8	2.54	0.43
2:L5:1091:C:H2'	2:L5:1092:G:H8	1.84	0.42
2:L5:1370:G:OP2	7:LC:48:ASN:ND2	2.39	0.42
2:L5:1973:G:H4'	48:Lt:117:ARG:NH2	2.31	0.42
2:L5:4637:OMG:H1'	2:L5:4637:OMG:HM23	1.68	0.42
8:LD:223:PHE:O	8:LD:227:ILE:HG12	2.19	0.42
18:LO:108:ILE:HD12	18:LO:160:ARG:CZ	2.49	0.42
19:LP:41:ILE:HG12	19:LP:99:GLU:OE2	2.19	0.42
34:Le:35:TRP:HH2	34:Le:55:MET:HG2	1.84	0.42
34:Le:92:ASN:C	34:Le:92:ASN:HD22	2.27	0.42
40:Lk:5:ILE:HD11	40:Lk:43:TYR:HB3	2.01	0.42
44:Lo:32:SER:C	44:Lo:34:TYR:H	2.26	0.42
49:SD:31:GLU:HA	49:SD:107:TYR:HE2	1.83	0.42
55:SR:13:ALA:O	55:SR:17:ILE:HG12	2.19	0.42
55:SR:27:ASP:HB3	55:SR:30:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SS:112:GLU:HG2	56:SS:115:LYS:HE3	2.01	0.42
66:SC:165:VAL:HG11	66:SC:217:ALA:HB1	2.01	0.42
78:SY:56:PHE:HE2	78:SY:82:ALA:HB1	1.84	0.42
82:S2:1047:C:H2'	82:S2:1048:G:O4'	2.19	0.42
82:S2:1271:C:H2'	82:S2:1272:OMC:O4'	2.19	0.42
2:L5:223:G:N7	7:LC:165:LYS:HE3	2.34	0.42
2:L5:455:C:O2'	2:L5:456:C:H5'	2.19	0.42
2:L5:662:C:H2'	2:L5:663:G:H8	1.84	0.42
2:L5:746:A:H2'	2:L5:747:A:C8	2.54	0.42
2:L5:2474:G:H2'	2:L5:2502:G:N2	2.34	0.42
2:L5:3654:G:O2'	2:L5:3693:U:OP1	2.34	0.42
2:L5:3752:C:O2'	2:L5:3776:G:H1'	2.20	0.42
2:L5:3883:U:H2'	2:L5:3884:PSU:C6	2.53	0.42
2:L5:4086:G:O6	11:LG:48:LYS:NZ	2.49	0.42
2:L5:4739:C:H2'	2:L5:4740:G:H5'	2.01	0.42
86:L5:5294:SPM:H31	86:L5:5294:SPM:H62	1.81	0.42
8:LD:181:PRO:HD2	8:LD:195:HIS:CD2	2.54	0.42
13:LI:39:LYS:HE3	13:LI:39:LYS:HB2	1.80	0.42
18:LO:62:MET:HE2	18:LO:64:THR:HB	2.00	0.42
23:LT:8:ARG:HH11	23:LT:52:MET:HE1	1.84	0.42
29:LZ:100:VAL:HG22	29:LZ:107:LYS:HA	2.01	0.42
32:Lc:57:LYS:HB2	32:Lc:57:LYS:HE3	1.82	0.42
46:Lr:6:GLN:O	46:Lr:10:VAL:HG22	2.19	0.42
50:SF:129:GLY:HA3	50:SF:136:ARG:NH1	2.35	0.42
52:SM:66:GLU:HA	52:SM:69:CYS:SG	2.59	0.42
53:SP:52:LYS:NZ	82:S2:1299:A:O2'	2.53	0.42
55:SR:33:ARG:HD3	55:SR:33:ARG:HA	1.78	0.42
57:ST:13:GLU:HB3	57:ST:16:ARG:HH21	1.83	0.42
71:SJ:121:LYS:HZ2	82:S2:528:A:H5'	1.84	0.42
72:SL:132:ARG:HD3	82:S2:114:G:H5'	2.00	0.42
79:Sa:41:ILE:HD12	79:Sa:68:TYR:CD2	2.54	0.42
82:S2:1208:A:H2'	82:S2:1209:A:C8	2.53	0.42
2:L5:135:G:N7	37:Lh:97:LYS:HE3	2.34	0.42
2:L5:189:G:H2'	2:L5:190:G:H8	1.84	0.42
2:L5:1197:C:H2'	2:L5:1198:G:C8	2.54	0.42
2:L5:1316:OMG:HM23	2:L5:1316:OMG:H1'	1.74	0.42
2:L5:1538:U:H2'	2:L5:1539:G:C8	2.54	0.42
2:L5:1825:A:H2'	2:L5:1826:G:H8	1.84	0.42
2:L5:1877:G:O6	31:Lb:10:HIS:NE2	2.49	0.42
2:L5:2041:A:N7	2:L5:4434:C:O2'	2.46	0.42
2:L5:2256:C:H2'	2:L5:2257:C:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2267:U:OP1	46:Lr:37:SER:HB2	2.19	0.42
2:L5:2318:G:N2	2:L5:2321:G:OP2	2.45	0.42
2:L5:2544:G:N1	4:L8:124:U:H5'	2.29	0.42
2:L5:3824:A:H3'	2:L5:3825:A2M:H8	2.01	0.42
2:L5:3870:C:H2'	2:L5:3871:A:H8	1.85	0.42
2:L5:3917:A:H2'	2:L5:3918:G:C8	2.52	0.42
2:L5:4092:G:N2	2:L5:4158:C:C2	2.87	0.42
2:L5:4524:G:N3	6:LB:252:ALA:HB1	2.34	0.42
5:LA:80:GLU:HB2	5:LA:170:ALA:HA	1.99	0.42
6:LB:29:VAL:HA	6:LB:220:ILE:HD13	2.01	0.42
7:LC:266:THR:HG22	7:LC:267:TRP:H	1.83	0.42
14:LJ:31:ASP:OD1	14:LJ:32:ARG:N	2.52	0.42
17:LN:97:SER:O	17:LN:100:SER:OG	2.34	0.42
24:LU:48:LYS:HG2	24:LU:53:ALA:HB2	2.01	0.42
49:SD:209:SER:HB3	55:SR:40:ILE:HG12	2.00	0.42
52:SM:58:GLU:HB2	82:S2:1285:G:N2	2.34	0.42
55:SR:96:ILE:HG21	64:SA:19:LEU:HB3	2.02	0.42
70:SI:44:HIS:NE2	82:S2:307:G:O6	2.52	0.42
76:SW:8:ALA:HA	76:SW:74:VAL:HG11	2.01	0.42
77:SX:105:PHE:CD1	77:SX:121:LYS:HB3	2.51	0.42
80:Sb:17:ARG:HH11	82:S2:1127:C:H4'	1.82	0.42
82:S2:809:A:H2'	82:S2:810:A:O4'	2.20	0.42
82:S2:1467:C:H2'	82:S2:1468:C:C6	2.54	0.42
82:S2:1845:A:H2'	82:S2:1846:G:C8	2.54	0.42
2:L5:408:A:O2'	2:L5:411:G:OP2	2.25	0.42
2:L5:676:C:H2'	2:L5:677:G:H8	1.84	0.42
2:L5:1094:G:O6	2:L5:1201:U:O2	2.36	0.42
2:L5:1947:U:C4	42:Lm:108:VAL:HG21	2.54	0.42
2:L5:2602:G:H2'	2:L5:2603:C:C6	2.54	0.42
2:L5:3656:A:O2'	2:L5:3747:A:O2'	2.34	0.42
2:L5:4301:U:OP2	2:L5:4303:C:N4	2.52	0.42
2:L5:4342:C:O3'	44:Lo:37:GLY:HA3	2.19	0.42
2:L5:4622:A:H4'	6:LB:13:SER:HB2	2.00	0.42
6:LB:154:LYS:HB2	6:LB:154:LYS:HE2	1.75	0.42
12:LH:27:VAL:HG12	12:LH:84:VAL:HG21	2.02	0.42
15:LL:55:ILE:O	15:LL:97:SER:OG	2.34	0.42
18:LO:155:THR:O	18:LO:158:GLU:HG2	2.19	0.42
20:LQ:22:ASP:HB3	20:LQ:25:LEU:HB3	2.00	0.42
21:LR:25:ASP:OD2	84:CI:72:ARG:CZ	2.67	0.42
29:LZ:115:LYS:O	29:LZ:119:GLU:HG3	2.19	0.42
48:Lt:61:LYS:HB3	48:Lt:74:VAL:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SS:27:ALA:HB2	56:SS:52:LEU:HD12	2.01	0.42
56:SS:67:VAL:O	56:SS:71:MET:HG2	2.20	0.42
62:Sf:139:HIS:O	62:Sf:147:THR:HA	2.19	0.42
65:SB:39:PHE:CD2	65:SB:74:LEU:HD22	2.54	0.42
66:SC:194:ARG:HD3	66:SC:196:ILE:HD11	2.01	0.42
68:SG:133:LEU:HD12	82:S2:65:C:C2	2.54	0.42
68:SG:199:THR:HG21	82:S2:126:G:H8	1.83	0.42
69:SH:63:PHE:HA	69:SH:95:ILE:O	2.20	0.42
70:SI:129:LEU:HD12	70:SI:129:LEU:HA	1.90	0.42
76:SW:125:ILE:HD12	76:SW:125:ILE:HA	1.83	0.42
82:S2:99:A2M:H8	82:S2:99:A2M:O5'	2.18	0.42
82:S2:458:A:H2'	82:S2:459:C:C6	2.55	0.42
82:S2:583:A:H3'	82:S2:584:A:H8	1.85	0.42
82:S2:1232:PSU:H2'	82:S2:1233:G:H8	1.84	0.42
83:Zt:52:G:HO2'	83:Zt:53:G:P	2.40	0.42
2:L5:749:G:N2	2:L5:912:G:O2'	2.46	0.42
2:L5:962:C:H1'	10:LF:32:ARG:NH1	2.34	0.42
2:L5:979:C:OP2	9:LE:66:LYS:HD3	2.20	0.42
2:L5:2015:U:H2'	2:L5:2016:C:O4'	2.18	0.42
2:L5:2749:C:H2'	2:L5:2750:G:H8	1.84	0.42
2:L5:4065:G:H2'	2:L5:4066:U:C6	2.54	0.42
2:L5:4392:OMG:N3	2:L5:4447:5MC:HM52	2.35	0.42
2:L5:4536:OMC:HM22	2:L5:4537:C:O4'	2.20	0.42
2:L5:4691:A:OP1	12:LH:75:SER:OG	2.34	0.42
2:L5:4859:C:O2'	18:LO:169:ARG:NH2	2.43	0.42
6:LB:80:GLU:OE2	6:LB:328:ASN:ND2	2.52	0.42
7:LC:315:LYS:HD2	10:LF:168:ALA:HB1	2.00	0.42
9:LE:108:LYS:NZ	9:LE:111:LYS:HA	2.35	0.42
18:LO:61:ARG:HA	18:LO:70:PRO:HD2	2.02	0.42
26:LW:73:ARG:NH2	82:S2:1748:G:O6	2.53	0.42
33:Ld:37:GLY:O	33:Ld:41:ARG:HG3	2.20	0.42
47:Ls:17:ILE:HG22	47:Ls:21:LEU:HD23	2.02	0.42
54:SQ:102:GLU:HB2	54:SQ:105:LYS:HE2	2.01	0.42
64:SA:61:ALA:O	64:SA:65:ILE:HG12	2.20	0.42
65:SB:39:PHE:HA	65:SB:75:GLN:OE1	2.19	0.42
66:SC:121:ARG:HH12	66:SC:123:ARG:CZ	2.33	0.42
67:SE:15:PRO:HG3	67:SE:39:ARG:HH11	1.84	0.42
67:SE:43:PRO:HG2	67:SE:46:ILE:HG12	2.00	0.42
67:SE:180:LEU:N	67:SE:231:GLY:O	2.52	0.42
76:SW:30:CYS:SG	76:SW:61:ILE:HD11	2.59	0.42
77:SX:90:CYS:HA	77:SX:93:PHE:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:SY:8:ARG:HH22	82:S2:835:C:H5''	1.83	0.42
78:SY:10:ARG:HA	82:S2:839:C:H41	1.84	0.42
81:Se:36:MET:HB3	81:Se:40:ARG:NH1	2.35	0.42
82:S2:652:U:H2'	82:S2:653:A:H8	1.85	0.42
82:S2:690:G:H3'	82:S2:690:G:N3	2.35	0.42
82:S2:695:C:H5	82:S2:737:G:H21	1.67	0.42
82:S2:1221:G:H2'	82:S2:1222:G:C8	2.54	0.42
82:S2:1265:A:O2'	82:S2:1327:G:OP2	2.19	0.42
82:S2:1539:U:H2'	82:S2:1540:G:H8	1.84	0.42
82:S2:1702:G:H2'	82:S2:1703:OMC:O4'	2.20	0.42
82:S2:1748:G:O6	82:S2:1786:U:O4	2.37	0.42
2:L5:99:A:H2'	2:L5:100:C:O2	2.19	0.42
2:L5:1669:A:H4'	2:L5:1685:G:N2	2.35	0.42
2:L5:1700:G:H5''	2:L5:1704:C:N4	2.35	0.42
2:L5:2624:G:OP1	84:CI:71:ARG:HD2	2.19	0.42
2:L5:2743:A:H2'	2:L5:2744:A:C8	2.54	0.42
2:L5:2897:G:H2'	2:L5:2898:G:H8	1.84	0.42
2:L5:4066:U:H2'	2:L5:4067:U:C6	2.55	0.42
2:L5:5002:U:H2'	2:L5:5003:U:C6	2.54	0.42
2:L5:5010:PSU:H2'	2:L5:5011:A:H8	1.84	0.42
5:LA:96:LEU:HD21	5:LA:107:MET:HG2	2.01	0.42
15:LL:23:ALA:HB3	17:LN:199:GLN:HA	2.01	0.42
19:LP:50:ASP:OD1	19:LP:55:LYS:HB2	2.19	0.42
26:LW:80:ARG:HH22	82:S2:167:G:H4'	1.83	0.42
49:SD:32:ASP:OD2	49:SD:58:VAL:HG13	2.20	0.42
57:ST:129:ARG:NH1	57:ST:133:ARG:HH12	2.17	0.42
65:SB:133:TYR:CG	65:SB:181:LEU:HD22	2.55	0.42
67:SE:121:TYR:OH	67:SE:235:TRP:O	2.27	0.42
78:SY:36:PRO:HD2	78:SY:39:GLU:OE2	2.19	0.42
82:S2:201:C:H3'	82:S2:202:G:H21	1.84	0.42
82:S2:543:C:H3'	82:S2:544:G:C8	2.53	0.42
82:S2:573:U:O2	82:S2:576:A2M:H8	2.20	0.42
82:S2:1182:A:C5	82:S2:1183:A:H1'	2.55	0.42
82:S2:1280:G:H2'	82:S2:1281:G:H8	1.85	0.42
2:L5:1086:C:H2'	2:L5:1087:A:H8	1.85	0.42
2:L5:1655:C:HO2'	2:L5:4391:G:HO2'	1.58	0.42
2:L5:1697:G:H22	2:L5:2084:C:P	2.42	0.42
2:L5:2399:G:HO2'	2:L5:2822:G:HO2'	1.68	0.42
2:L5:3868:G:N2	2:L5:3900:G:O2'	2.49	0.42
2:L5:4883:C:H2'	2:L5:4884:G:H8	1.85	0.42
2:L5:4987:C:P	6:LB:116:ARG:HH22	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LH:115:ARG:HD3	12:LH:123:ILE:HD12	2.01	0.42
36:Lg:50:PRO:HG3	45:Lp:61:MET:HE3	2.01	0.42
47:Ls:30:VAL:HG23	47:Ls:189:ILE:HA	2.02	0.42
51:SK:53:LYS:HE2	51:SK:53:LYS:HB2	1.83	0.42
52:SM:82:ASN:OD1	52:SM:83:LYS:N	2.52	0.42
66:SC:165:VAL:HG12	66:SC:244:ILE:HG23	2.01	0.42
70:SI:25:ARG:HH22	82:S2:434:G:P	2.42	0.42
73:SN:5:HIS:HB3	73:SN:117:LEU:HD13	2.02	0.42
77:SX:66:ILE:HD12	81:Se:3:HIS:CE1	2.55	0.42
82:S2:33:G:O2'	82:S2:564:A:O2'	2.34	0.42
82:S2:876:C:H2'	82:S2:877:C:C6	2.54	0.42
82:S2:1018:U:H2'	82:S2:1019:C:C6	2.55	0.42
82:S2:1597:C:H4'	82:S2:1603:G:O6	2.19	0.42
82:S2:1616:U:O2'	82:S2:1661:A:N3	2.43	0.42
82:S2:1788:A:H2'	82:S2:1789:G:O4'	2.20	0.42
82:S2:1798:C:H2'	82:S2:1799:G:O4'	2.20	0.42
2:L5:137:G:H2'	2:L5:138:G:C8	2.50	0.42
2:L5:239:C:OP1	28:LY:46:SER:OG	2.31	0.42
2:L5:665:C:H1'	2:L5:668:C:H41	1.83	0.42
2:L5:4153:C:H2'	2:L5:4154:G:H8	1.83	0.42
2:L5:4466:C:H2'	2:L5:4467:A:H8	1.85	0.42
2:L5:4871:C:N4	22:LS:171:ARG:O	2.52	0.42
13:LI:177:ASN:HB2	13:LI:180:GLU:CD	2.45	0.42
18:LO:107:GLY:HA2	18:LO:157:GLU:OE2	2.19	0.42
33:Ld:75:LYS:HE3	33:Ld:79:ASN:O	2.20	0.42
53:SP:41:GLN:HE22	53:SP:113:GLY:C	2.28	0.42
54:SQ:110:ASP:OD1	54:SQ:111:ILE:HD12	2.20	0.42
55:SR:10:LYS:HG2	55:SR:53:TYR:CE2	2.55	0.42
63:Sg:52:TYR:CE2	63:Sg:309:VAL:HG21	2.55	0.42
69:SH:97:GLN:C	69:SH:98:ARG:HD2	2.45	0.42
78:SY:4:THR:H	78:SY:32:LYS:HZ3	1.68	0.42
82:S2:441:C:H2'	82:S2:442:C:C6	2.54	0.42
82:S2:1092:G:H2'	82:S2:1093:A:H8	1.85	0.42
83:Zt:60:U:H2'	83:Zt:61:C:H5	1.84	0.42
2:L5:1985:G:H2'	2:L5:1986:U:C6	2.55	0.42
2:L5:1998:A:H2'	2:L5:1999:A:C4	2.55	0.42
2:L5:2020:U:O3'	47:Ls:57:LYS:HA	2.19	0.42
4:L8:66:A:H2'	4:L8:67:U:H6	1.85	0.42
5:LA:116:LEU:HD12	5:LA:117:GLU:H	1.85	0.42
15:LL:136:LYS:HE2	15:LL:136:LYS:HB3	1.91	0.42
17:LN:200:LEU:HD22	17:LN:204:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LP:94:MET:SD	19:LP:148:MET:HE3	2.60	0.42
26:LW:56:ARG:HE	26:LW:61:LYS:CB	2.33	0.42
29:LZ:5:MET:HE2	29:LZ:82:PRO:HB3	2.01	0.42
51:SK:20:VAL:HG22	51:SK:70:TYR:HA	2.01	0.42
61:Sd:54:LYS:NZ	82:S2:1482:C:OP1	2.53	0.42
63:Sg:20:GLN:HG2	63:Sg:69:VAL:H	1.84	0.42
63:Sg:85:GLY:HA2	63:Sg:108:VAL:HG23	2.01	0.42
64:SA:122:LEU:HD12	64:SA:122:LEU:HA	1.85	0.42
65:SB:68:GLU:HB3	65:SB:83:LYS:NZ	2.34	0.42
67:SE:149:TYR:CD2	68:SG:205:GLU:HB3	2.54	0.42
76:SW:71:LYS:NZ	82:S2:1156:U:OP1	2.53	0.42
82:S2:946:U:H2'	82:S2:947:G:H8	1.85	0.42
82:S2:1099:G:H22	82:S2:1133:A:H2	1.68	0.42
83:Zt:5:G:H2'	83:Zt:6:G:O4'	2.20	0.42
83:Zt:72:C:C2	83:Zt:73:G:C8	3.07	0.42
84:CI:63:ARG:HD2	84:CI:63:ARG:HA	1.85	0.42
2:L5:727:C:H5''	10:LF:69:ILE:HG21	2.02	0.42
2:L5:2448:G:H2'	2:L5:2449:A:C8	2.55	0.42
2:L5:2580:U:O2'	29:LZ:79:HIS:ND1	2.45	0.42
2:L5:4507:A:H2'	2:L5:4508:C:C6	2.54	0.42
2:L5:4517:A:OP2	6:LB:2:SER:N	2.53	0.42
86:L5:5264:SPM:HN0	86:L5:5264:SPM:H132	1.65	0.42
5:LA:30:ARG:NH1	5:LA:36:GLU:OE1	2.53	0.42
5:LA:114:CYS:N	5:LA:165:VAL:O	2.53	0.42
8:LD:258:LYS:C	8:LD:259:LYS:HD2	2.45	0.42
15:LL:48:PRO:HG3	37:Lh:118:LYS:HE2	2.02	0.42
17:LN:178:HIS:HA	17:LN:181:HIS:NE2	2.35	0.42
47:Ls:148:SER:N	47:Ls:151:THR:O	2.50	0.42
53:SP:98:ASN:O	82:S2:1240:A:N6	2.50	0.42
57:ST:105:GLN:HA	57:ST:108:GLU:CD	2.45	0.42
63:Sg:32:LEU:HA	63:Sg:42:MET:HA	2.02	0.42
65:SB:70:SER:OG	65:SB:71:LEU:N	2.52	0.42
68:SG:85:ARG:O	68:SG:87:ARG:NH1	2.53	0.42
69:SH:137:SER:HB3	69:SH:162:GLN:HE21	1.85	0.42
69:SH:159:ASP:OD1	69:SH:160:LYS:N	2.53	0.42
82:S2:146:G:H2'	82:S2:147:A:H8	1.85	0.42
82:S2:1373:C:H2'	82:S2:1374:C:C6	2.55	0.42
2:L5:705:G:H2'	2:L5:706:C:H6	1.84	0.41
2:L5:1217:G:C2	2:L5:1218:G:C5	3.08	0.41
2:L5:1736:A:H2'	2:L5:1737:A:O4'	2.20	0.41
2:L5:2032:U:H2'	2:L5:2033:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:3722:G:H2'	2:L5:3723:A:C8	2.53	0.41
2:L5:3896:C:H1'	6:LB:268:ARG:NH2	2.35	0.41
2:L5:3930:U:H3	2:L5:4180:G:H1	1.67	0.41
2:L5:4727:A:H2'	2:L5:4728:U:O4'	2.20	0.41
4:L8:52:A:H2'	4:L8:53:G:H8	1.85	0.41
7:LC:33:ARG:HG3	7:LC:122:TYR:CE2	2.54	0.41
22:LS:16:CYS:SG	22:LS:54:MET:HG2	2.60	0.41
30:La:73:VAL:HB	30:La:108:TYR:CD2	2.55	0.41
48:Lt:64:ILE:HB	48:Lt:71:ILE:HG13	2.02	0.41
50:SF:42:LYS:HG3	50:SF:43:GLU:OE1	2.20	0.41
51:SK:8:ARG:NH2	82:S2:1314:U:O2'	2.52	0.41
51:SK:85:LEU:HD23	51:SK:86:PRO:O	2.20	0.41
52:SM:89:VAL:HG13	52:SM:91:LEU:HD23	2.01	0.41
55:SR:109:LEU:HD11	64:SA:52:LYS:HB2	2.01	0.41
59:SZ:50:PHE:HE2	59:SZ:87:ALA:HB2	1.84	0.41
62:Sf:108:VAL:HB	62:Sf:112:GLY:HA2	2.02	0.41
68:SG:159:ARG:NH1	82:S2:76:U:O2'	2.53	0.41
70:SI:81:VAL:HA	70:SI:102:VAL:HG12	2.02	0.41
72:SL:18:GLN:HG2	72:SL:33:LEU:HD11	2.01	0.41
82:S2:321:C:H2'	82:S2:322:C:C6	2.55	0.41
82:S2:452:G:H2'	82:S2:453:C:H6	1.85	0.41
82:S2:946:U:H2'	82:S2:947:G:C8	2.55	0.41
82:S2:1447:G:H2'	82:S2:1448:A:C8	2.55	0.41
82:S2:1537:A:H2'	82:S2:1538:C:H6	1.84	0.41
83:Zt:27:U:H2'	83:Zt:28:C:H6	1.85	0.41
83:Zt:32:C:H2'	83:Zt:33:U:C2	2.55	0.41
1:Pt:40:C:H2'	1:Pt:41:G:H8	1.84	0.41
2:L5:161:G:H2'	2:L5:162:A:C8	2.55	0.41
2:L5:368:C:O4'	7:LC:83:GLY:HA3	2.20	0.41
2:L5:1241:C:O2	31:Lb:115:GLY:HA2	2.21	0.41
2:L5:1241:C:H1'	31:Lb:119:CYS:HA	2.02	0.41
2:L5:1354:A:OP2	20:LQ:106:THR:HG21	2.20	0.41
2:L5:1479:G:H2'	2:L5:1480:C:C6	2.54	0.41
19:LP:32:THR:HA	19:LP:58:VAL:HG21	2.02	0.41
20:LQ:57:ASN:HA	20:LQ:143:ARG:HD2	2.01	0.41
27:LX:89:LYS:HE2	27:LX:137:TYR:CD1	2.55	0.41
30:La:71:PRO:HG2	30:La:108:TYR:HA	2.02	0.41
48:Lt:147:HIS:HA	48:Lt:148:PRO:HD3	1.79	0.41
50:SF:100:ILE:HB	50:SF:178:ILE:HD11	2.00	0.41
51:SK:14:LEU:HD22	51:SK:35:LEU:HD23	2.02	0.41
52:SM:49:LEU:O	52:SM:110:VAL:HA	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SS:64:VAL:O	56:SS:68:ILE:HG12	2.20	0.41
57:ST:129:ARG:HG3	82:S2:1416:C:OP1	2.19	0.41
63:Sg:26:GLN:NE2	63:Sg:73:SER:O	2.51	0.41
64:SA:81:ASN:OD1	64:SA:81:ASN:N	2.54	0.41
65:SB:223:PHE:HE1	65:SB:228:LEU:HD22	1.85	0.41
66:SC:183:LYS:HA	66:SC:195:LEU:O	2.20	0.41
76:SW:60:LYS:NZ	82:S2:921:G:N7	2.68	0.41
82:S2:17:C:H2'	82:S2:18:C:H6	1.84	0.41
82:S2:907:G:H2'	82:S2:908:A:H8	1.85	0.41
82:S2:1409:A:H2'	82:S2:1410:C:C6	2.55	0.41
2:L5:374:G:OP2	39:Lj:56:ARG:NH1	2.44	0.41
2:L5:398:A2M:H1'	2:L5:398:A2M:HM'3	1.62	0.41
2:L5:2654:C:H2'	2:L5:2655:C:C6	2.55	0.41
2:L5:4492:U:H5''	2:L5:4493:PSU:H5''	2.02	0.41
2:L5:4678:G:N2	2:L5:4713:G:H1'	2.35	0.41
2:L5:5010:PSU:H2'	2:L5:5011:A:C8	2.55	0.41
5:LA:131:GLY:N	5:LA:169:VAL:HG13	2.34	0.41
10:LF:208:LEU:HD23	10:LF:208:LEU:HA	1.95	0.41
12:LH:91:LYS:HD2	12:LH:183:GLU:OE2	2.21	0.41
20:LQ:66:MET:HE1	20:LQ:86:ILE:HD13	2.01	0.41
34:Le:90:MET:HE3	46:Lr:113:ARG:HG3	2.01	0.41
38:Li:44:ILE:HD13	38:Li:44:ILE:HA	1.91	0.41
46:Lr:113:ARG:O	46:Lr:117:ILE:HD12	2.21	0.41
51:SK:1:MET:HE1	51:SK:47:LYS:HB2	2.01	0.41
57:ST:42:HIS:NE2	57:ST:43:LYS:HE3	2.35	0.41
57:ST:78:ILE:HD11	82:S2:1587:G:C5	2.56	0.41
63:Sg:289:LEU:HD11	63:Sg:298:LEU:HD21	2.03	0.41
66:SC:65:LYS:HD2	66:SC:273:LEU:HD13	2.02	0.41
67:SE:188:ASN:ND2	67:SE:219:ALA:O	2.52	0.41
77:SX:60:LYS:H	77:SX:114:ASP:HB2	1.84	0.41
78:SY:121:ALA:O	78:SY:125:VAL:HG22	2.20	0.41
82:S2:14:C:H2'	82:S2:15:U:C6	2.56	0.41
82:S2:419:G:N2	82:S2:661:U:O2	2.53	0.41
82:S2:737:G:H2'	82:S2:738:C:H4'	2.02	0.41
82:S2:830:A:OP2	82:S2:846:G:N2	2.45	0.41
82:S2:960:U:O2'	82:S2:962:A:N7	2.44	0.41
82:S2:1731:A:H2'	82:S2:1732:G:H8	1.85	0.41
2:L5:321:U:H2'	2:L5:322:C:C6	2.55	0.41
2:L5:921:C:H2'	2:L5:922:C:C6	2.55	0.41
2:L5:1191:C:H2'	2:L5:1192:C:H6	1.85	0.41
2:L5:1563:A:H2'	2:L5:1564:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:1777:C:H2'	2:L5:1778:C:C6	2.56	0.41
2:L5:2521:G:H2'	2:L5:2522:G:C8	2.55	0.41
2:L5:2621:A:OP1	24:LU:80:LYS:NZ	2.47	0.41
2:L5:2664:G:H4'	2:L5:2677:G:H4'	2.01	0.41
2:L5:4195:G:OP1	2:L5:4221:C:O2'	2.35	0.41
2:L5:4688:C:H2'	2:L5:4689:PSU:C6	2.55	0.41
5:LA:171:GLY:O	45:Lp:68:ALA:HB2	2.19	0.41
17:LN:149:GLN:HE22	37:Lh:102:LEU:HD21	1.86	0.41
20:LQ:110:ARG:HG3	20:LQ:120:ILE:HD12	2.02	0.41
31:Lb:43:MET:HE3	31:Lb:47:LYS:NZ	2.36	0.41
39:Lj:2:THR:HB	39:Lj:6:SER:HB2	2.01	0.41
46:Lr:49:VAL:HG23	46:Lr:64:ILE:HG22	2.02	0.41
51:SK:15:LEU:HG	51:SK:71:LEU:HD11	2.01	0.41
66:SC:263:LYS:HA	66:SC:267:GLN:HE21	1.84	0.41
82:S2:27:A2M:H2'	82:S2:28:U:O4'	2.20	0.41
82:S2:119:U:H2'	82:S2:120:U:H6	1.84	0.41
82:S2:367:U:H4'	82:S2:371:A:C8	2.56	0.41
82:S2:752:G:OP2	82:S2:752:G:N2	2.49	0.41
82:S2:1395:C:H2'	82:S2:1396:A:O4'	2.21	0.41
82:S2:1401:A:H2'	82:S2:1402:A:C8	2.55	0.41
82:S2:1673:U:H2'	82:S2:1674:G:O4'	2.20	0.41
82:S2:1739:C:H2'	82:S2:1740:C:C6	2.55	0.41
2:L5:497:G:N2	2:L5:498:C:H41	2.18	0.41
2:L5:1278:C:H2'	2:L5:1279:A:O4'	2.20	0.41
2:L5:1289:C:H2'	2:L5:1290:G:H8	1.86	0.41
2:L5:1461:C:H2'	2:L5:1462:A:H8	1.85	0.41
2:L5:5006:U:H4'	2:L5:5007:A:H5'	2.03	0.41
15:LL:110:LEU:O	15:LL:114:VAL:HG13	2.20	0.41
21:LR:80:LYS:HA	21:LR:80:LYS:HD2	1.88	0.41
22:LS:50:GLN:OE1	22:LS:51:LEU:HD22	2.20	0.41
30:La:110:LYS:HD3	30:La:112:LEU:HD21	2.02	0.41
31:Lb:101:HIS:HB3	31:Lb:104:LEU:HB2	2.03	0.41
47:Ls:14:PHE:CZ	47:Ls:63:LYS:HD2	2.56	0.41
49:SD:4:GLN:O	82:S2:1578:U:O2'	2.37	0.41
57:ST:89:PRO:HG3	82:S2:1529:C:H4'	2.03	0.41
63:Sg:101:PHE:HB3	63:Sg:132:TRP:CZ3	2.56	0.41
66:SC:128:VAL:HG11	66:SC:155:ILE:HG13	2.02	0.41
67:SE:246:LEU:HD13	67:SE:250:GLU:HG2	2.03	0.41
70:SI:4:SER:HB3	70:SI:24:LYS:HD3	2.02	0.41
71:SJ:129:LEU:HD21	71:SJ:159:PHE:HE1	1.86	0.41
77:SX:34:THR:HG21	82:S2:1189:A:H4'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:S2:1275:G:H22	82:S2:1506:A:P	2.42	0.41
2:L5:515:C:H41	2:L5:647:G:N2	2.18	0.41
2:L5:1411:C:H2'	2:L5:1412:G:C8	2.56	0.41
2:L5:1662:C:H2'	2:L5:1663:C:H6	1.85	0.41
2:L5:1703:C:HO2'	2:L5:1704:C:C5'	2.34	0.41
2:L5:1733:G:N3	2:L5:4214:A:H2'	2.36	0.41
2:L5:3648:A:H1'	2:L5:3785:A2M:N6	2.35	0.41
3:L7:111:C:H2'	3:L7:112:U:O4'	2.21	0.41
6:LB:117:ARG:HG2	6:LB:180:LEU:HD23	2.02	0.41
6:LB:294:LYS:HD3	6:LB:298:LEU:HD11	2.02	0.41
10:LF:86:GLU:OE2	23:LT:136:ARG:NH2	2.53	0.41
12:LH:89:ARG:HD3	12:LH:91:LYS:HE3	2.03	0.41
22:LS:19:THR:C	22:LS:21:LYS:H	2.28	0.41
37:Lh:113:LEU:HD23	37:Lh:113:LEU:HA	1.86	0.41
49:SD:72:VAL:HG22	51:SK:20:VAL:HG11	2.02	0.41
54:SQ:132:PHE:HB2	58:SU:77:TRP:CD1	2.56	0.41
55:SR:44:LYS:NZ	82:S2:1450:G:H5''	2.35	0.41
57:ST:102:ARG:HD3	57:ST:102:ARG:HA	1.89	0.41
59:SZ:101:SER:OG	59:SZ:108:ILE:N	2.52	0.41
63:Sg:106:LYS:HB3	63:Sg:125:ARG:HB2	2.02	0.41
65:SB:71:LEU:HD22	65:SB:82:ARG:HD2	2.03	0.41
66:SC:224:THR:O	82:S2:2:A:O2'	2.39	0.41
67:SE:31:PRO:HB3	67:SE:43:PRO:HB3	2.02	0.41
82:S2:24:C:O2'	82:S2:25:A:O5'	2.39	0.41
82:S2:429:C:H2'	82:S2:430:C:C6	2.55	0.41
82:S2:943:U:C2	82:S2:944:A:C8	3.09	0.41
82:S2:1233:G:N3	82:S2:1252:C:O2'	2.38	0.41
82:S2:1805:G:H2'	82:S2:1806:A:C8	2.56	0.41
1:Pt:6:C:H2'	1:Pt:7:G:C8	2.55	0.41
2:L5:163:A:H2'	2:L5:164:G:C8	2.55	0.41
2:L5:958:G:N2	9:LE:124:LYS:HB3	2.36	0.41
2:L5:1241:C:H1'	31:Lb:120:ARG:H	1.86	0.41
2:L5:1645:C:H2'	2:L5:1646:A:H8	1.86	0.41
2:L5:1677:PSU:H4'	2:L5:1680:G:C2	2.55	0.41
2:L5:1998:A:P	47:Ls:13:TYR:HE1	2.44	0.41
2:L5:2295:C:H2'	2:L5:2296:G:H8	1.86	0.41
2:L5:2520:C:H2'	2:L5:2521:G:C8	2.55	0.41
2:L5:3598:C:H2'	2:L5:3599:A:C8	2.56	0.41
2:L5:3723:A:OP2	38:Li:68:ARG:NH2	2.30	0.41
2:L5:4456:OMC:HM23	2:L5:4456:OMC:H1'	1.82	0.41
2:L5:4460:U:H2'	2:L5:4461:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:4601:U:OP2	2:L5:4609:G:N1	2.51	0.41
2:L5:4616:A:H2'	2:L5:4617:G:O4'	2.21	0.41
2:L5:4893:A:H3'	2:L5:4894:A:H8	1.85	0.41
11:LG:144:THR:O	11:LG:148:GLU:HG3	2.21	0.41
26:LW:4:GLU:HG2	26:LW:12:LYS:HZ2	1.86	0.41
47:Ls:14:PHE:CE2	47:Ls:63:LYS:HD2	2.55	0.41
49:SD:1:MET:SD	49:SD:3:VAL:N	2.81	0.41
50:SF:100:ILE:HD11	50:SF:108:PRO:HB3	2.02	0.41
57:ST:134:ILE:HA	57:ST:137:GLN:HG3	2.03	0.41
63:Sg:21:ILE:HD13	63:Sg:33:SER:HB3	2.02	0.41
67:SE:184:THR:N	67:SE:224:ASN:O	2.33	0.41
68:SG:133:LEU:HD12	82:S2:65:C:C4	2.56	0.41
69:SH:119:SER:OG	69:SH:120:ARG:NH1	2.54	0.41
70:SI:141:ARG:NE	82:S2:191:A:OP1	2.54	0.41
70:SI:191:GLU:O	72:SL:19:ASN:ND2	2.54	0.41
77:SX:52:LEU:N	77:SX:71:ARG:O	2.42	0.41
82:S2:113:G:O6	82:S2:290:U:H1'	2.21	0.41
82:S2:301:A:H2'	82:S2:302:A:O4'	2.21	0.41
82:S2:548:C:H2'	82:S2:549:C:H6	1.85	0.41
82:S2:651:PSU:H2'	82:S2:652:U:C6	2.56	0.41
82:S2:900:C:H5'	82:S2:901:G:N7	2.35	0.41
82:S2:964:A:H2'	82:S2:965:U:H6	1.85	0.41
82:S2:1098:C:H2'	82:S2:1099:G:C8	2.56	0.41
82:S2:1739:C:H2'	82:S2:1740:C:H6	1.85	0.41
2:L5:71:C:H1'	15:LL:62:PRO:O	2.21	0.41
2:L5:441:G:H2'	2:L5:442:G:H8	1.85	0.41
2:L5:666:G:H4'	2:L5:667:A:C6	2.56	0.41
2:L5:4130:C:H2'	2:L5:4131:G:H8	1.86	0.41
2:L5:4164:C:H2'	2:L5:4165:C:C6	2.56	0.41
2:L5:4458:C:H2'	2:L5:4459:U:C6	2.56	0.41
3:L7:4:U:H2'	3:L7:5:A:H8	1.86	0.41
4:L8:46:G:O2'	4:L8:61:A:N1	2.49	0.41
6:LB:17:LEU:HA	6:LB:17:LEU:HD23	1.80	0.41
6:LB:201:LEU:HD23	6:LB:201:LEU:HA	1.88	0.41
14:LJ:24:ILE:HG13	14:LJ:40:LEU:HD11	2.03	0.41
18:LO:110:PRO:N	18:LO:111:PRO:HD2	2.35	0.41
20:LQ:10:ASP:OD1	20:LQ:11:ARG:N	2.53	0.41
23:LT:122:LYS:HG3	23:LT:124:THR:HG22	2.01	0.41
33:Ld:33:ILE:HD11	33:Ld:41:ARG:HB3	2.02	0.41
33:Ld:123:ASP:OD1	33:Ld:124:GLU:N	2.49	0.41
35:Lf:45:LYS:NZ	35:Lf:108:SER:HA	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Ls:19:GLN:O	47:Ls:23:ASP:HB2	2.21	0.41
53:SP:18:ARG:NH2	82:S2:1612:G:OP1	2.54	0.41
56:SS:36:VAL:HG22	56:SS:40:TYR:HD2	1.86	0.41
64:SA:18:PHE:CZ	64:SA:177:MET:HE2	2.56	0.41
64:SA:19:LEU:HD23	64:SA:24:HIS:CE1	2.56	0.41
64:SA:148:CYS:SG	64:SA:160:ALA:HB1	2.61	0.41
71:SJ:121:LYS:NZ	82:S2:528:A:H5'	2.36	0.41
73:SN:61:ALA:HB1	82:S2:1016:U:H6	1.85	0.41
78:SY:39:GLU:HA	78:SY:42:GLU:CD	2.46	0.41
82:S2:107:A:H2'	82:S2:108:G:C8	2.55	0.41
82:S2:349:A:H2'	82:S2:350:C:C6	2.55	0.41
82:S2:635:G:H2'	82:S2:636:C:C6	2.56	0.41
82:S2:1013:U:H2'	82:S2:1014:G:H8	1.85	0.41
82:S2:1179:G:N2	82:S2:1182:A:OP2	2.48	0.41
82:S2:1348:G:H2'	82:S2:1349:G:H8	1.85	0.41
82:S2:1804:U:H2'	82:S2:1805:G:H8	1.85	0.41
82:S2:1850:MA6:H8	82:S2:1850:MA6:O5'	2.20	0.41
2:L5:347:A:H2'	2:L5:348:G:C8	2.55	0.41
2:L5:492:U:H2'	2:L5:493:G:C8	2.56	0.41
2:L5:655:C:OP1	7:LC:268:ARG:NH1	2.54	0.41
2:L5:1344:C:H1'	15:LL:10:LEU:HD11	2.02	0.41
2:L5:1368:A:H2'	2:L5:1369:C:O4'	2.21	0.41
2:L5:1772:C:H2'	2:L5:1773:U:C6	2.56	0.41
2:L5:2412:A:H2'	2:L5:2413:U:C6	2.56	0.41
2:L5:3621:A:C8	2:L5:4642:U:H1'	2.56	0.41
2:L5:4233:A:OP2	44:Lo:97:LYS:HD2	2.20	0.41
2:L5:4452:U:OP2	2:L5:4522:G:N1	2.33	0.41
2:L5:4459:U:H2'	2:L5:4460:U:C6	2.56	0.41
2:L5:4460:U:H2'	2:L5:4461:C:H6	1.85	0.41
2:L5:4585:U:H2'	2:L5:4586:G:H8	1.86	0.41
2:L5:4691:A:O3'	12:LH:71:ARG:HD3	2.21	0.41
87:L5:5287:SPD:H92	4:L8:138:C:OP1	2.20	0.41
12:LH:26:ILE:HG12	12:LH:35:ARG:HE	1.86	0.41
18:LO:190:ASP:OD1	18:LO:191:LYS:N	2.54	0.41
24:LU:111:GLU:OE1	24:LU:113:ARG:HG3	2.21	0.41
29:LZ:99:ASP:HB2	29:LZ:102:ARG:HE	1.85	0.41
32:Lc:22:MET:O	32:Lc:23:LYS:HG2	2.21	0.41
44:Lo:63:THR:HG22	44:Lo:89:LYS:HG2	2.02	0.41
46:Lr:17:LEU:HD21	46:Lr:19:LYS:HD2	2.03	0.41
52:SM:35:ILE:N	82:S2:1285:G:OP2	2.45	0.41
55:SR:81:ARG:O	64:SA:85:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:ST:126:GLN:HB2	57:ST:129:ARG:NH2	2.32	0.41
63:Sg:68:ASP:HB3	63:Sg:111:VAL:HG22	2.03	0.41
64:SA:120:ARG:NH2	66:SC:267:GLN:HB3	2.35	0.41
66:SC:196:ILE:HB	66:SC:223:TYR:HB2	2.03	0.41
67:SE:28:ALA:O	82:S2:496:C:H4'	2.21	0.41
67:SE:124:CYS:HB3	67:SE:141:THR:HB	2.03	0.41
69:SH:81:ARG:O	69:SH:85:LYS:HG3	2.21	0.41
71:SJ:144:ILE:HG21	82:S2:824:C:C2	2.56	0.41
77:SX:87:ASN:HB3	77:SX:134:TYR:CE1	2.56	0.41
78:SY:105:LYS:NZ	82:S2:507:G:O6	2.53	0.41
79:Sa:95:ARG:O	82:S2:1866:A:O2'	2.34	0.41
82:S2:24:C:O2'	82:S2:25:A:H8	2.03	0.41
82:S2:46:A:H61	82:S2:433:A:H2	1.69	0.41
82:S2:448:A:H4'	82:S2:449:A:H5''	2.02	0.41
82:S2:815:U:C2	82:S2:816:A:C8	3.09	0.41
82:S2:1467:C:H2'	82:S2:1468:C:H6	1.86	0.41
82:S2:1495:G:H2'	82:S2:1496:U:C6	2.55	0.41
82:S2:1600:G:O2'	82:S2:1601:A:H4'	2.20	0.41
2:L5:280:G:OP2	17:LN:44:ARG:NH1	2.51	0.41
2:L5:1346:C:H2'	2:L5:1347:G:C8	2.55	0.41
2:L5:2568:C:H2'	2:L5:2569:G:H8	1.85	0.41
2:L5:2871:A:H2'	2:L5:2872:C:O4'	2.21	0.41
2:L5:4126:C:OP1	11:LG:37:LYS:NZ	2.55	0.41
2:L5:4943:A:OP1	9:LE:155:GLY:N	2.41	0.41
3:L7:48:G:OP1	8:LD:226:TYR:OH	2.34	0.41
5:LA:142:GLU:C	5:LA:144:LYS:H	2.29	0.41
13:LI:152:LEU:HB3	13:LI:165:ILE:HD12	2.01	0.41
14:LJ:18:ARG:HD2	14:LJ:135:GLY:HA3	2.02	0.41
14:LJ:120:ASP:HB3	14:LJ:123:ILE:HB	2.03	0.41
32:Lc:38:ILE:HG21	32:Lc:63:TYR:HB3	2.02	0.41
48:Lt:114:ARG:NH2	48:Lt:119:ARG:HH21	2.19	0.41
52:SM:63:LYS:O	52:SM:66:GLU:HG3	2.21	0.41
56:SS:137:LYS:HE3	82:S2:1234:C:N4	2.36	0.41
57:ST:83:GLN:HE21	57:ST:85:ASN:H	1.68	0.41
63:Sg:104:HIS:NE2	63:Sg:122:SER:OG	2.50	0.41
63:Sg:215:GLN:HE22	63:Sg:217:MET:HB2	1.85	0.41
64:SA:77:ILE:HA	64:SA:99:ILE:O	2.21	0.41
70:SI:56:ARG:HA	70:SI:180:GLY:HA2	2.02	0.41
70:SI:141:ARG:HA	70:SI:141:ARG:CZ	2.51	0.41
72:SL:21:LYS:HD2	72:SL:21:LYS:HA	1.84	0.41
82:S2:1320:G:H2'	82:S2:1321:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:120:A:N1	2:L5:148:C:O2'	2.47	0.40
2:L5:184:U:O2'	2:L5:189:G:O4'	2.39	0.40
2:L5:452:A:H62	2:L5:1293:G:H5''	1.86	0.40
2:L5:455:C:C2'	2:L5:456:C:H5'	2.52	0.40
2:L5:1443:A:H2'	2:L5:1444:G:C8	2.56	0.40
2:L5:1494:U:H2'	2:L5:1495:G:H8	1.85	0.40
2:L5:3910:C:H2'	2:L5:3911:C:H6	1.86	0.40
2:L5:5015:G:H2'	2:L5:5016:A:C2	2.56	0.40
10:LF:147:LEU:O	10:LF:151:ASN:ND2	2.47	0.40
12:LH:137:SER:HB2	12:LH:143:GLU:OE1	2.21	0.40
21:LR:19:LYS:HB2	21:LR:19:LYS:HE2	1.89	0.40
21:LR:35:ALA:HA	21:LR:40:GLN:OE1	2.21	0.40
28:LY:109:LEU:HD22	28:LY:115:ARG:NH2	2.36	0.40
41:L1:9:ILE:HD12	41:L1:9:ILE:HA	1.94	0.40
50:SF:198:ARG:O	50:SF:201:LYS:HG3	2.21	0.40
57:ST:88:MET:HE3	57:ST:88:MET:HB3	2.00	0.40
65:SB:167:LYS:HB2	65:SB:167:LYS:HE2	1.88	0.40
68:SG:13:GLN:NE2	82:S2:153:G:N3	2.69	0.40
68:SG:188:LYS:O	68:SG:192:ILE:HG12	2.21	0.40
70:SI:69:SER:HG	70:SI:70:GLU:CD	2.27	0.40
70:SI:117:TYR:HE2	70:SI:156:ALA:HA	1.86	0.40
72:SL:80:MET:HE2	72:SL:122:ILE:HG13	2.03	0.40
82:S2:373:G:H2'	82:S2:374:G:H8	1.85	0.40
82:S2:964:A:H2'	82:S2:965:U:C6	2.56	0.40
82:S2:1176:G:C6	82:S2:1177:PSU:C2	3.10	0.40
2:L5:113:A:H2'	2:L5:114:G:O4'	2.21	0.40
2:L5:307:A:N3	2:L5:310:G:O2'	2.53	0.40
2:L5:426:A:H2'	2:L5:427:A:H8	1.86	0.40
2:L5:1097:C:H2'	2:L5:1098:G:H8	1.86	0.40
2:L5:1281:G:C6	9:LE:128:HIS:HB2	2.55	0.40
2:L5:2325:C:OP1	34:Le:101:HIS:N	2.46	0.40
2:L5:2695:A:OP1	40:Lk:35:LYS:NZ	2.33	0.40
2:L5:2696:A:H62	40:Lk:35:LYS:NZ	2.18	0.40
2:L5:3819:G:H2'	2:L5:3820:G:H8	1.86	0.40
2:L5:4508:C:N3	2:L5:4512:U:H5	2.19	0.40
3:L7:3:C:H2'	3:L7:4:U:H6	1.86	0.40
3:L7:23:A:H2'	3:L7:24:C:C6	2.56	0.40
4:L8:64:U:C2	4:L8:65:A:C8	3.10	0.40
11:LG:229:ARG:NH2	11:LG:232:GLU:OE2	2.54	0.40
19:LP:50:ASP:OD2	19:LP:56:GLN:HG3	2.21	0.40
19:LP:125:MET:HB2	19:LP:141:SER:OG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LR:163:ARG:NH1	82:S2:871:U:H3	2.19	0.40
24:LU:37:ALA:O	24:LU:40:GLU:HG3	2.20	0.40
24:LU:116:GLN:O	84:CI:74:LYS:CB	2.70	0.40
46:Lr:49:VAL:HG21	46:Lr:97:ILE:HD11	2.03	0.40
49:SD:134:CYS:SG	49:SD:135:GLU:N	2.95	0.40
50:SF:88:MET:O	50:SF:91:ARG:HG2	2.21	0.40
53:SP:93:MET:HE1	53:SP:106:GLU:OE1	2.22	0.40
54:SQ:67:ASP:OD2	54:SQ:69:ARG:NH1	2.54	0.40
65:SB:168:MET:HB2	65:SB:197:ILE:HD13	2.02	0.40
68:SG:6:SER:O	68:SG:112:VAL:HA	2.22	0.40
70:SI:117:TYR:CE2	70:SI:156:ALA:HA	2.56	0.40
74:SO:42:VAL:HG11	74:SO:78:ALA:HA	2.04	0.40
77:SX:105:PHE:CE2	77:SX:112:VAL:HB	2.56	0.40
82:S2:396:U:O2'	82:S2:401:A:O2'	2.29	0.40
82:S2:1567:G:H2'	82:S2:1568:C:C6	2.57	0.40
82:S2:1597:C:H4'	82:S2:1603:G:C6	2.56	0.40
1:Pt:2:U:H2'	1:Pt:3:C:C6	2.57	0.40
2:L5:92:C:OP2	2:L5:4341:C:O2'	2.26	0.40
2:L5:513:U:O2	2:L5:515:C:H3'	2.20	0.40
2:L5:965:G:H1'	2:L5:2093:A:N1	2.37	0.40
2:L5:1304:C:H2'	2:L5:1305:C:C6	2.56	0.40
2:L5:1431:C:H2'	2:L5:1432:G:O4'	2.21	0.40
2:L5:1468:C:H2'	2:L5:1469:C:H6	1.87	0.40
2:L5:1961:G:H8	47:Ls:59:THR:HG21	1.86	0.40
2:L5:2079:G:H2'	2:L5:2080:U:H6	1.86	0.40
2:L5:2632:PSU:H2'	2:L5:2633:U:C6	2.56	0.40
2:L5:2823:G:N7	21:LR:20:LYS:HD3	2.35	0.40
2:L5:4111:U:H2'	2:L5:4112:C:C5	2.57	0.40
2:L5:4578:G:H2'	2:L5:4579:PSU:H6	1.86	0.40
2:L5:4965:U:H4'	2:L5:4966:A:H5'	2.04	0.40
6:LB:214:ASP:OD2	6:LB:362:LYS:HA	2.22	0.40
14:LJ:94:LEU:HD12	14:LJ:166:PHE:CZ	2.56	0.40
19:LP:137:ASN:HD22	19:LP:137:ASN:HA	1.65	0.40
23:LT:52:MET:HG2	23:LT:95:HIS:CE1	2.57	0.40
32:Lc:48:LEU:HD13	32:Lc:57:LYS:HG3	2.03	0.40
34:Le:98:GLU:HG2	34:Le:123:THR:OG1	2.21	0.40
51:SK:51:SER:OG	51:SK:55:ARG:NH1	2.55	0.40
53:SP:92:SER:O	53:SP:93:MET:HE2	2.21	0.40
53:SP:134:GLY:H	82:S2:1236:G:H4'	1.85	0.40
57:ST:6:VAL:HG12	57:ST:135:ALA:HB2	2.03	0.40
60:Sc:17:VAL:HA	60:Sc:30:VAL:HG12	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SA:180:ARG:HH12	64:SA:184:ARG:HH11	1.70	0.40
66:SC:185:THR:OG1	82:S2:1155:U:OP1	2.35	0.40
70:SI:87:ASN:HB3	70:SI:90:LEU:HG	2.04	0.40
70:SI:121:LEU:HD21	70:SI:166:PHE:CD2	2.57	0.40
70:SI:148:LYS:O	70:SI:151:GLU:HG3	2.21	0.40
77:SX:17:ARG:NH1	82:S2:658:U:H1'	2.36	0.40
82:S2:96:C:H2'	82:S2:97:U:C6	2.57	0.40
82:S2:116:OMU:HM23	82:S2:116:OMU:H1'	1.78	0.40
82:S2:344:U:H2'	82:S2:345:U:H6	1.85	0.40
82:S2:432:G:H2'	82:S2:433:A:H8	1.86	0.40
82:S2:1310:U:H2'	82:S2:1311:C:C5	2.57	0.40
2:L5:256:G:H2'	2:L5:257:C:C6	2.56	0.40
2:L5:288:G:H2'	2:L5:289:C:C6	2.56	0.40
2:L5:510:U:OP1	15:LL:163:LYS:HE3	2.21	0.40
2:L5:1743:A:O4'	8:LD:15:ARG:HD2	2.21	0.40
2:L5:2400:G:H21	36:Lg:6:THR:HG22	1.86	0.40
2:L5:3641:U:H5	2:L5:3646:A:N7	2.18	0.40
2:L5:4094:G:H22	2:L5:4115:G:P	2.41	0.40
2:L5:4633:G:O2'	2:L5:4635:A:OP2	2.29	0.40
2:L5:5026:U:H4'	2:L5:5027:C:O4'	2.22	0.40
3:L7:24:C:H2'	3:L7:25:G:O4'	2.22	0.40
3:L7:46:C:H2'	3:L7:47:G:H8	1.87	0.40
27:LX:95:THR:HG22	27:LX:139:ARG:HG3	2.03	0.40
44:Lo:83:LEU:HD23	44:Lo:83:LEU:HA	1.85	0.40
48:Lt:24:ALA:H	48:Lt:48:LYS:NZ	2.20	0.40
48:Lt:130:LYS:HA	48:Lt:130:LYS:HE2	2.04	0.40
50:SF:36:GLN:NE2	50:SF:37:ASP:HB3	2.36	0.40
56:SS:105:ASN:O	56:SS:108:ARG:HG2	2.21	0.40
64:SA:67:ALA:HB2	75:SV:37:ALA:HB2	2.03	0.40
65:SB:171:ILE:HG21	65:SB:197:ILE:HG12	2.02	0.40
69:SH:53:VAL:HG21	69:SH:172:THR:HG22	2.03	0.40
69:SH:58:LYS:HA	69:SH:58:LYS:HD2	1.78	0.40
70:SI:132:GLU:O	70:SI:136:ILE:HG12	2.21	0.40
71:SJ:33:GLY:HA3	81:Se:38:TYR:CD1	2.57	0.40
77:SX:90:CYS:HA	77:SX:93:PHE:HD2	1.86	0.40
81:Se:5:SER:HB3	81:Se:8:ARG:HH21	1.86	0.40
82:S2:17:C:O2'	82:S2:1194:A:N1	2.49	0.40
82:S2:627:OMU:H6	82:S2:627:OMU:H5''	2.03	0.40
82:S2:1088:U:H4'	82:S2:1089:G:OP2	2.22	0.40
2:L5:1248:C:H2'	2:L5:1249:C:C6	2.57	0.40
2:L5:1503:A:H1'	2:L5:1504:G:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L5:2029:A:H2'	2:L5:2030:A:H8	1.86	0.40
2:L5:2422:OMC:HM23	2:L5:2422:OMC:H1'	1.91	0.40
2:L5:3599:A:H2'	2:L5:3600:G:C8	2.55	0.40
2:L5:3610:A:H2'	2:L5:3611:A:C8	2.56	0.40
2:L5:4725:C:OP1	6:LB:103:LYS:NZ	2.55	0.40
2:L5:4759:C:O2	18:LO:165:LYS:NZ	2.36	0.40
2:L5:4886:C:H2'	2:L5:4887:C:H6	1.87	0.40
2:L5:4911:A:OP2	6:LB:100:ARG:HD3	2.22	0.40
7:LC:143:ARG:HG2	7:LC:182:LYS:HD2	2.03	0.40
7:LC:334:THR:HG21	10:LF:51:TYR:OH	2.22	0.40
8:LD:79:TYR:O	8:LD:82:GLU:HG2	2.22	0.40
9:LE:164:PHE:CE1	9:LE:173:LEU:HD12	2.57	0.40
18:LO:190:ASP:O	18:LO:194:GLU:HG2	2.21	0.40
37:Lh:52:LYS:HA	37:Lh:52:LYS:HD3	1.73	0.40
37:Lh:104:THR:HG23	37:Lh:107:GLN:H	1.87	0.40
50:SF:40:ALA:H	50:SF:68:ILE:HG23	1.86	0.40
50:SF:61:PHE:CZ	60:Sc:51:ARG:HG3	2.57	0.40
51:SK:20:VAL:HG13	51:SK:69:TRP:O	2.21	0.40
62:Sf:125:GLU:HG2	62:Sf:126:CYS:N	2.36	0.40
65:SB:92:GLN:HG3	65:SB:97:LEU:HD11	2.04	0.40
66:SC:74:LYS:HD3	66:SC:74:LYS:HA	1.87	0.40
68:SG:136:LYS:HB3	82:S2:170:A:O5'	2.21	0.40
76:SW:2:VAL:N	82:S2:1091:C:O2'	2.47	0.40
78:SY:9:THR:H	82:S2:837:A:N6	2.19	0.40
80:Sb:56:CYS:SG	80:Sb:63:LEU:HD11	2.62	0.40
82:S2:109:PSU:H2'	82:S2:110:U:C6	2.57	0.40
82:S2:591:U:H5''	82:S2:593:C:H5'	2.03	0.40
83:Zt:1:G:H2'	83:Zt:2:C:C6	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	LA	246/248 (99%)	233 (95%)	13 (5%)	0	100	100
6	LB	400/402 (100%)	374 (94%)	26 (6%)	0	100	100
7	LC	366/368 (100%)	352 (96%)	14 (4%)	0	100	100
8	LD	291/293 (99%)	280 (96%)	11 (4%)	0	100	100
9	LE	236/240 (98%)	219 (93%)	17 (7%)	0	100	100
10	LF	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
11	LG	239/241 (99%)	226 (95%)	13 (5%)	0	100	100
12	LH	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
13	LI	211/213 (99%)	198 (94%)	13 (6%)	0	100	100
14	LJ	168/176 (96%)	158 (94%)	10 (6%)	0	100	100
15	LL	208/210 (99%)	199 (96%)	9 (4%)	0	100	100
16	LM	137/139 (99%)	129 (94%)	8 (6%)	0	100	100
17	LN	201/203 (99%)	197 (98%)	4 (2%)	0	100	100
18	LO	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
19	LP	151/153 (99%)	144 (95%)	7 (5%)	0	100	100
20	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
21	LR	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
22	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
23	LT	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
24	LU	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
25	LV	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
26	LW	112/118 (95%)	107 (96%)	5 (4%)	0	100	100
27	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
28	LY	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
29	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
30	La	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
31	Lb	105/109 (96%)	101 (96%)	4 (4%)	0	100	100
32	Lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
33	Ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
34	Le	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
35	Lf	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
36	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
38	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
39	Lj	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
40	Lk	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
41	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
42	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
43	Ln	22/24 (92%)	22 (100%)	0	0	100	100
44	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
45	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
46	Lr	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
47	Ls	194/196 (99%)	182 (94%)	12 (6%)	0	100	100
48	Lt	128/141 (91%)	108 (84%)	20 (16%)	0	100	100
49	SD	225/227 (99%)	211 (94%)	14 (6%)	0	100	100
50	SF	187/189 (99%)	174 (93%)	13 (7%)	0	100	100
51	SK	96/98 (98%)	88 (92%)	8 (8%)	0	100	100
52	SM	120/122 (98%)	110 (92%)	9 (8%)	1 (1%)	16	47
53	SP	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
54	SQ	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
55	SR	133/135 (98%)	124 (93%)	8 (6%)	1 (1%)	16	47
56	SS	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
57	ST	141/143 (99%)	138 (98%)	3 (2%)	0	100	100
58	SU	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
59	SZ	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
60	Sc	62/64 (97%)	57 (92%)	5 (8%)	0	100	100
61	Sd	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
62	Sf	65/67 (97%)	59 (91%)	6 (9%)	0	100	100
63	Sg	311/313 (99%)	290 (93%)	21 (7%)	0	100	100
64	SA	219/221 (99%)	204 (93%)	15 (7%)	0	100	100
65	SB	212/214 (99%)	198 (93%)	14 (7%)	0	100	100
66	SC	218/222 (98%)	204 (94%)	14 (6%)	0	100	100
67	SE	260/262 (99%)	254 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	SG	235/237 (99%)	221 (94%)	14 (6%)	0	100	100
69	SH	182/186 (98%)	167 (92%)	15 (8%)	0	100	100
70	SI	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
71	SJ	183/185 (99%)	172 (94%)	10 (6%)	1 (0%)	24	58
72	SL	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
73	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
74	SO	135/140 (96%)	124 (92%)	11 (8%)	0	100	100
75	SV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
76	SW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
77	SX	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
78	SY	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
79	Sa	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
80	Sb	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
81	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
84	CI	29/31 (94%)	29 (100%)	0	0	100	100
All	All	11672/11860 (98%)	11053 (95%)	616 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
55	SR	129	LYS
71	SJ	138	ARG
52	SM	94	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	LA	190/190 (100%)	190 (100%)	0	100	100
6	LB	348/348 (100%)	348 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	LC	306/306 (100%)	306 (100%)	0	100	100
8	LD	246/247 (100%)	246 (100%)	0	100	100
9	LE	212/212 (100%)	212 (100%)	0	100	100
10	LF	194/194 (100%)	194 (100%)	0	100	100
11	LG	203/205 (99%)	203 (100%)	0	100	100
12	LH	169/169 (100%)	169 (100%)	0	100	100
13	LI	180/180 (100%)	180 (100%)	0	100	100
14	LJ	143/148 (97%)	143 (100%)	0	100	100
15	LL	176/176 (100%)	176 (100%)	0	100	100
16	LM	118/118 (100%)	118 (100%)	0	100	100
17	LN	171/171 (100%)	171 (100%)	0	100	100
18	LO	173/173 (100%)	173 (100%)	0	100	100
19	LP	134/134 (100%)	134 (100%)	0	100	100
20	LQ	164/164 (100%)	164 (100%)	0	100	100
21	LR	166/166 (100%)	166 (100%)	0	100	100
22	LS	156/156 (100%)	156 (100%)	0	100	100
23	LT	139/139 (100%)	139 (100%)	0	100	100
24	LU	91/91 (100%)	91 (100%)	0	100	100
25	LV	101/101 (100%)	101 (100%)	0	100	100
26	LW	95/97 (98%)	95 (100%)	0	100	100
27	LX	108/108 (100%)	108 (100%)	0	100	100
28	LY	124/124 (100%)	124 (100%)	0	100	100
29	LZ	117/117 (100%)	117 (100%)	0	100	100
30	La	120/120 (100%)	120 (100%)	0	100	100
31	Lb	88/90 (98%)	88 (100%)	0	100	100
32	Lc	83/83 (100%)	83 (100%)	0	100	100
33	Ld	98/98 (100%)	98 (100%)	0	100	100
34	Le	114/114 (100%)	114 (100%)	0	100	100
35	Lf	88/88 (100%)	88 (100%)	0	100	100
36	Lg	98/98 (100%)	98 (100%)	0	100	100
37	Lh	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Li	86/86 (100%)	86 (100%)	0	100	100
39	Lj	73/73 (100%)	73 (100%)	0	100	100
40	Lk	64/64 (100%)	64 (100%)	0	100	100
41	Ll	47/47 (100%)	47 (100%)	0	100	100
42	Lm	48/48 (100%)	48 (100%)	0	100	100
43	Ln	23/23 (100%)	23 (100%)	0	100	100
44	Lo	93/93 (100%)	93 (100%)	0	100	100
45	Lp	74/74 (100%)	74 (100%)	0	100	100
46	Lr	109/109 (100%)	109 (100%)	0	100	100
47	Ls	162/164 (99%)	162 (100%)	0	100	100
48	Lt	107/115 (93%)	107 (100%)	0	100	100
49	SD	190/190 (100%)	190 (100%)	0	100	100
50	SF	159/159 (100%)	159 (100%)	0	100	100
51	SK	89/89 (100%)	89 (100%)	0	100	100
52	SM	102/104 (98%)	102 (100%)	0	100	100
53	SP	107/107 (100%)	107 (100%)	0	100	100
54	SQ	119/119 (100%)	119 (100%)	0	100	100
55	SR	122/122 (100%)	122 (100%)	0	100	100
56	SS	126/126 (100%)	126 (100%)	0	100	100
57	ST	113/113 (100%)	113 (100%)	0	100	100
58	SU	94/94 (100%)	94 (100%)	0	100	100
59	SZ	66/66 (100%)	66 (100%)	0	100	100
60	Sc	57/57 (100%)	57 (100%)	0	100	100
61	Sd	48/48 (100%)	48 (100%)	0	100	100
62	Sf	60/60 (100%)	60 (100%)	0	100	100
63	Sg	272/272 (100%)	272 (100%)	0	100	100
64	SA	183/183 (100%)	183 (100%)	0	100	100
65	SB	195/195 (100%)	195 (100%)	0	100	100
66	SC	186/188 (99%)	186 (100%)	0	100	100
67	SE	224/224 (100%)	224 (100%)	0	100	100
68	SG	207/207 (100%)	207 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	SH	166/166 (100%)	165 (99%)	1 (1%)	78	88
70	SI	178/178 (100%)	178 (100%)	0	100	100
71	SJ	161/161 (100%)	161 (100%)	0	100	100
72	SL	137/137 (100%)	137 (100%)	0	100	100
73	SN	130/130 (100%)	130 (100%)	0	100	100
74	SO	107/110 (97%)	107 (100%)	0	100	100
75	SV	67/67 (100%)	67 (100%)	0	100	100
76	SW	112/112 (100%)	112 (100%)	0	100	100
77	SX	113/113 (100%)	112 (99%)	1 (1%)	70	85
78	SY	113/113 (100%)	113 (100%)	0	100	100
79	Sa	89/89 (100%)	89 (100%)	0	100	100
80	Sb	75/75 (100%)	75 (100%)	0	100	100
81	Se	47/47 (100%)	47 (100%)	0	100	100
84	CI	25/25 (100%)	25 (100%)	0	100	100
All	All	10147/10176 (100%)	10145 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	SH	73	GLN
77	SX	127	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
5	LA	8	GLN
5	LA	97	ASN
6	LB	68	ASN
6	LB	186	ASN
6	LB	289	GLN
7	LC	215	ASN
7	LC	310	HIS
7	LC	329	ASN
8	LD	122	GLN
8	LD	244	HIS
8	LD	267	ASN

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Mol	Chain	Res	Type
9	LE	135	GLN
9	LE	227	HIS
10	LF	80	ASN
10	LF	116	GLN
10	LF	119	ASN
11	LG	64	GLN
11	LG	227	ASN
12	LH	98	HIS
13	LI	112	GLN
14	LJ	23	ASN
14	LJ	65	ASN
16	LM	34	ASN
17	LN	37	HIS
17	LN	87	HIS
17	LN	117	ASN
19	LP	75	GLN
19	LP	97	ASN
19	LP	137	ASN
22	LS	37	HIS
23	LT	98	HIS
26	LW	79	GLN
26	LW	96	GLN
27	LX	111	GLN
28	LY	14	ASN
28	LY	18	HIS
28	LY	20	ASN
28	LY	61	HIS
30	La	34	ASN
30	La	60	HIS
30	La	66	ASN
32	Lc	72	HIS
34	Le	52	GLN
34	Le	92	ASN
37	Lh	20	GLN
37	Lh	68	ASN
38	Li	26	HIS
39	Lj	13	ASN
41	Ll	17	GLN
41	Ll	33	ASN
45	Lp	33	GLN
47	Ls	71	ASN
47	Ls	179	ASN

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Mol	Chain	Res	Type
47	Ls	190	GLN
48	Lt	65	GLN
48	Lt	66	ASN
49	SD	145	GLN
50	SF	95	HIS
50	SF	101	HIS
50	SF	118	ASN
51	SK	32	HIS
51	SK	42	ASN
53	SP	24	GLN
56	SS	135	HIS
57	ST	83	GLN
59	SZ	64	ASN
60	Sc	29	GLN
61	Sd	5	GLN
63	Sg	117	ASN
63	Sg	159	ASN
63	Sg	215	GLN
63	Sg	272	GLN
63	Sg	285	GLN
64	SA	50	ASN
64	SA	84	GLN
65	SB	118	GLN
65	SB	158	HIS
65	SB	208	HIS
66	SC	277	HIS
67	SE	50	ASN
67	SE	216	ASN
68	SG	81	HIS
68	SG	110	ASN
68	SG	227	GLN
69	SH	73	GLN
69	SH	162	GLN
69	SH	165	ASN
72	SL	19	ASN
75	SV	35	ASN
76	SW	64	ASN
77	SX	87	ASN
81	Se	3	HIS
81	Se	15	GLN
81	Se	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Pt	72/74 (97%)	14 (19%)	0
2	L5	3643/3655 (99%)	744 (20%)	14 (0%)
3	L7	119/120 (99%)	8 (6%)	0
4	L8	155/156 (99%)	25 (16%)	0
82	S2	1714/1740 (98%)	378 (22%)	3 (0%)
83	Zt	74/75 (98%)	38 (51%)	0
All	All	5777/5820 (99%)	1207 (20%)	17 (0%)

All (1207) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Pt	9	A
1	Pt	13	U
1	Pt	19	G
1	Pt	21	A
1	Pt	46	G
1	Pt	47	U
1	Pt	48	C
1	Pt	49	C
1	Pt	58	A
1	Pt	61	C
1	Pt	67	G
1	Pt	72	C
1	Pt	74	C
1	Pt	76	A
2	L5	25	A
2	L5	30	C
2	L5	39	A
2	L5	42	A
2	L5	48	G
2	L5	56	A
2	L5	59	A
2	L5	64	A
2	L5	65	A
2	L5	73	A
2	L5	91	G
2	L5	104	G
2	L5	108	A
2	L5	109	G
2	L5	110	C
2	L5	119	G

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Mol	Chain	Res	Type
2	L5	120	A
2	L5	132	G
2	L5	133	C
2	L5	134	G
2	L5	135	G
2	L5	139	G
2	L5	144	G
2	L5	145	G
2	L5	159	C
2	L5	165	A
2	L5	166	C
2	L5	172	C
2	L5	173	C
2	L5	182	G
2	L5	183	C
2	L5	184	U
2	L5	185	C
2	L5	186	G
2	L5	187	U
2	L5	188	G
2	L5	189	G
2	L5	200	U
2	L5	209	U
2	L5	210	C
2	L5	216	C
2	L5	218	A
2	L5	220	C
2	L5	234	G
2	L5	237	G
2	L5	255	C
2	L5	256	G
2	L5	261	G
2	L5	263	G
2	L5	264	C
2	L5	265	C
2	L5	266	C
2	L5	267	G
2	L5	275	C
2	L5	276	C
2	L5	280	G
2	L5	281	U
2	L5	297	U

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Mol	Chain	Res	Type
2	L5	306	A
2	L5	315	G
2	L5	316	U
2	L5	340	C
2	L5	362	A
2	L5	373	G
2	L5	387	G
2	L5	388	A
2	L5	396	A
2	L5	398	A2M
2	L5	399	G
2	L5	407	A
2	L5	409	G
2	L5	410	A
2	L5	411	G
2	L5	412	G
2	L5	413	G
2	L5	415	G
2	L5	449	C
2	L5	450	G
2	L5	452	A
2	L5	453	G
2	L5	454	U
2	L5	456	C
2	L5	457	G
2	L5	467	U
2	L5	468	U
2	L5	484	U
2	L5	485	C
2	L5	486	C
2	L5	489	C
2	L5	493	G
2	L5	494	U
2	L5	497	G
2	L5	498	C
2	L5	499	G
2	L5	500	G
2	L5	502	C
2	L5	503	C
2	L5	504	G
2	L5	509	A
2	L5	510	U

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Mol	Chain	Res	Type
2	L5	512	U
2	L5	513	U
2	L5	514	U
2	L5	518	G
2	L5	519	C
2	L5	643	C
2	L5	645	G
2	L5	646	G
2	L5	654	C
2	L5	655	C
2	L5	656	C
2	L5	657	C
2	L5	658	C
2	L5	659	G
2	L5	665	C
2	L5	666	G
2	L5	667	A
2	L5	668	C
2	L5	672	C
2	L5	673	C
2	L5	685	C
2	L5	686	A
2	L5	687	U
2	L5	696	C
2	L5	704	C
2	L5	731	G
2	L5	738	C
2	L5	739	G
2	L5	742	G
2	L5	746	A
2	L5	759	G
2	L5	904	C
2	L5	905	C
2	L5	906	C
2	L5	913	U
2	L5	914	U
2	L5	915	A
2	L5	917	A
2	L5	923	C
2	L5	924	C
2	L5	932	A
2	L5	933	G

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Mol	Chain	Res	Type
2	L5	936	C
2	L5	941	C
2	L5	943	A
2	L5	944	A
2	L5	945	U
2	L5	946	C
2	L5	956	A
2	L5	958	G
2	L5	959	G
2	L5	960	A
2	L5	961	G
2	L5	962	C
2	L5	965	G
2	L5	966	A
2	L5	967	C
2	L5	969	C
2	L5	970	G
2	L5	982	U
2	L5	985	C
2	L5	1070	G
2	L5	1072	C
2	L5	1075	G
2	L5	1076	C
2	L5	1082	C
2	L5	1083	U
2	L5	1168	G
2	L5	1170	G
2	L5	1171	G
2	L5	1172	C
2	L5	1173	G
2	L5	1179	U
2	L5	1180	C
2	L5	1181	C
2	L5	1182	C
2	L5	1183	C
2	L5	1184	A
2	L5	1187	G
2	L5	1202	C
2	L5	1203	G
2	L5	1210	C
2	L5	1211	G
2	L5	1214	C

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Mol	Chain	Res	Type
2	L5	1215	C
2	L5	1216	C
2	L5	1218	G
2	L5	1219	G
2	L5	1222	A
2	L5	1245	C
2	L5	1246	G
2	L5	1253	G
2	L5	1254	A
2	L5	1257	A
2	L5	1258	G
2	L5	1259	G
2	L5	1262	G
2	L5	1266	G
2	L5	1267	C
2	L5	1269	G
2	L5	1271	G
2	L5	1272	C
2	L5	1273	G
2	L5	1280	C
2	L5	1284	G
2	L5	1287	G
2	L5	1293	G
2	L5	1294	A
2	L5	1295	C
2	L5	1296	G
2	L5	1301	C
2	L5	1314	C
2	L5	1326	A2M
2	L5	1339	U
2	L5	1344	C
2	L5	1354	A
2	L5	1359	G
2	L5	1365	C
2	L5	1366	G
2	L5	1367	C
2	L5	1381	U
2	L5	1387	A
2	L5	1394	G
2	L5	1397	A
2	L5	1404	G
2	L5	1407	C

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Mol	Chain	Res	Type
2	L5	1409	C
2	L5	1410	U
2	L5	1411	C
2	L5	1414	C
2	L5	1417	C
2	L5	1420	A
2	L5	1437	C
2	L5	1439	C
2	L5	1441	C
2	L5	1443	A
2	L5	1444	G
2	L5	1446	C
2	L5	1447	C
2	L5	1482	G
2	L5	1483	C
2	L5	1497	A
2	L5	1498	G
2	L5	1502	G
2	L5	1517	G
2	L5	1523	A
2	L5	1524	A2M
2	L5	1534	A2M
2	L5	1537	A
2	L5	1547	A
2	L5	1562	G
2	L5	1564	A
2	L5	1566	C
2	L5	1578	U
2	L5	1591	U
2	L5	1596	U
2	L5	1597	G
2	L5	1624	G
2	L5	1625	OMG
2	L5	1631	A
2	L5	1633	G
2	L5	1634	A
2	L5	1640	C
2	L5	1641	G
2	L5	1642	A
2	L5	1654	G
2	L5	1661	C
2	L5	1676	C

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Mol	Chain	Res	Type
2	L5	1677	PSU
2	L5	1678	C
2	L5	1699	A
2	L5	1700	G
2	L5	1701	A
2	L5	1702	C
2	L5	1704	C
2	L5	1705	G
2	L5	1706	A
2	L5	1717	C
2	L5	1718	C
2	L5	1719	A
2	L5	1729	A
2	L5	1731	C
2	L5	1742	A
2	L5	1750	G
2	L5	1755	C
2	L5	1757	U
2	L5	1758	G
2	L5	1761	G
2	L5	1762	C
2	L5	1763	C
2	L5	1764	G
2	L5	1765	A
2	L5	1766	A
2	L5	1767	A
2	L5	1768	C
2	L5	1769	G
2	L5	1770	A
2	L5	1771	U
2	L5	1787	A
2	L5	1804	A
2	L5	1806	G
2	L5	1810	G
2	L5	1821	G
2	L5	1822	U
2	L5	1833	G
2	L5	1834	U
2	L5	1836	G
2	L5	1837	A
2	L5	1842	G
2	L5	1855	G

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Mol	Chain	Res	Type
2	L5	1869	G
2	L5	1882	U
2	L5	1892	A
2	L5	1897	A
2	L5	1917	A
2	L5	1918	U
2	L5	1919	G
2	L5	1920	C
2	L5	1921	C
2	L5	1922	G
2	L5	1925	G
2	L5	1931	C
2	L5	1932	A
2	L5	1936	C
2	L5	1940	G
2	L5	1948	G
2	L5	1951	G
2	L5	1961	G
2	L5	1962	A
2	L5	1974	U
2	L5	1975	G
2	L5	1978	C
2	L5	1980	U
2	L5	1981	G
2	L5	1982	G
2	L5	1984	A
2	L5	1985	G
2	L5	1986	U
2	L5	1989	G
2	L5	1990	A
2	L5	1991	A
2	L5	1993	C
2	L5	1997	U
2	L5	1998	A
2	L5	1999	A
2	L5	2001	G
2	L5	2002	A
2	L5	2003	G
2	L5	2004	U
2	L5	2011	C
2	L5	2012	A
2	L5	2014	C

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Mol	Chain	Res	Type
2	L5	2017	A
2	L5	2018	C
2	L5	2024	G
2	L5	2025	A
2	L5	2026	A
2	L5	2034	G
2	L5	2046	G
2	L5	2048	U
2	L5	2055	G
2	L5	2056	G
2	L5	2069	A
2	L5	2084	C
2	L5	2085	G
2	L5	2092	G
2	L5	2093	A
2	L5	2095	A
2	L5	2096	G
2	L5	2097	U
2	L5	2098	G
2	L5	2101	C
2	L5	2102	G
2	L5	2107	C
2	L5	2112	G
2	L5	2250	C
2	L5	2252	G
2	L5	2256	C
2	L5	2258	C
2	L5	2289	C
2	L5	2300	A
2	L5	2301	G
2	L5	2306	G
2	L5	2313	A
2	L5	2316	G
2	L5	2331	G
2	L5	2333	G
2	L5	2348	G
2	L5	2351	OMC
2	L5	2360	A
2	L5	2364	OMG
2	L5	2382	A
2	L5	2383	C
2	L5	2389	A

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Mol	Chain	Res	Type
2	L5	2395	A
2	L5	2397	G
2	L5	2401	A2M
2	L5	2417	A
2	L5	2425	U
2	L5	2464	C
2	L5	2465	C
2	L5	2469	C
2	L5	2471	G
2	L5	2474	G
2	L5	2475	G
2	L5	2478	C
2	L5	2479	G
2	L5	2483	G
2	L5	2484	A
2	L5	2485	U
2	L5	2487	G
2	L5	2488	C
2	L5	2489	C
2	L5	2490	U
2	L5	2491	C
2	L5	2494	U
2	L5	2504	C
2	L5	2505	C
2	L5	2506	G
2	L5	2511	A
2	L5	2513	A
2	L5	2519	U
2	L5	2529	A
2	L5	2536	A
2	L5	2537	A
2	L5	2544	G
2	L5	2546	G
2	L5	2547	G
2	L5	2554	U
2	L5	2555	G
2	L5	2556	G
2	L5	2560	C
2	L5	2565	A
2	L5	2567	G
2	L5	2573	A
2	L5	2583	C

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Mol	Chain	Res	Type
2	L5	2587	A
2	L5	2589	C
2	L5	2600	A
2	L5	2627	C
2	L5	2653	C
2	L5	2658	G
2	L5	2662	G
2	L5	2669	C
2	L5	2676	A
2	L5	2687	U
2	L5	2694	G
2	L5	2695	A
2	L5	2696	A
2	L5	2703	G
2	L5	2706	G
2	L5	2707	U
2	L5	2708	U
2	L5	2710	C
2	L5	2711	G
2	L5	2712	G
2	L5	2721	G
2	L5	2724	G
2	L5	2726	G
2	L5	2739	C
2	L5	2742	G
2	L5	2743	A
2	L5	2746	A
2	L5	2754	G
2	L5	2761	U
2	L5	2762	G
2	L5	2763	U
2	L5	2769	U
2	L5	2770	C
2	L5	2788	U
2	L5	2790	U
2	L5	2806	A
2	L5	2826	U
2	L5	2827	G
2	L5	2838	G
2	L5	2855	G
2	L5	2867	C
2	L5	2877	G

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Mol	Chain	Res	Type
2	L5	2895	A
2	L5	2900	U
2	L5	2901	G
2	L5	2902	G
2	L5	2903	G
2	L5	2904	U
2	L5	2905	C
2	L5	2906	G
2	L5	2907	G
2	L5	2908	U
2	L5	3588	C
2	L5	3590	G
2	L5	3591	C
2	L5	3594	C
2	L5	3595	U
2	L5	3596	A
2	L5	3597	G
2	L5	3604	A
2	L5	3605	C
2	L5	3616	U
2	L5	3617	G
2	L5	3626	G
2	L5	3635	A
2	L5	3644	U
2	L5	3646	A
2	L5	3648	A
2	L5	3662	A
2	L5	3670	C
2	L5	3673	C
2	L5	3674	G
2	L5	3691	G
2	L5	3701	OMC
2	L5	3710	G
2	L5	3711	A
2	L5	3713	U
2	L5	3726	A
2	L5	3727	A
2	L5	3748	A
2	L5	3753	G
2	L5	3760	A
2	L5	3770	U
2	L5	3774	A

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Mol	Chain	Res	Type
2	L5	3775	A
2	L5	3776	G
2	L5	3777	G
2	L5	3778	U
2	L5	3784	A
2	L5	3785	A2M
2	L5	3786	U
2	L5	3792	OMG
2	L5	3811	G
2	L5	3814	U
2	L5	3817	A
2	L5	3819	G
2	L5	3824	A
2	L5	3838	U
2	L5	3839	G
2	L5	3840	U
2	L5	3867	A2M
2	L5	3877	A
2	L5	3878	C
2	L5	3879	G
2	L5	3885	G
2	L5	3892	U
2	L5	3897	G
2	L5	3901	A
2	L5	3905	A
2	L5	3906	A
2	L5	3907	G
2	L5	3908	A
2	L5	3915	U
2	L5	3923	A
2	L5	3930	U
2	L5	3938	G
2	L5	3939	G
2	L5	3942	A
2	L5	3945	A
2	L5	3947	A
2	L5	3949	A
2	L5	3950	U
2	L5	3952	A
2	L5	3953	G
2	L5	4057	C
2	L5	4058	U

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Mol	Chain	Res	Type
2	L5	4059	C
2	L5	4061	G
2	L5	4062	A
2	L5	4064	C
2	L5	4065	G
2	L5	4068	U
2	L5	4076	G
2	L5	4084	G
2	L5	4088	C
2	L5	4093	G
2	L5	4095	G
2	L5	4097	G
2	L5	4099	G
2	L5	4101	C
2	L5	4104	G
2	L5	4105	A
2	L5	4108	G
2	L5	4111	U
2	L5	4114	C
2	L5	4115	G
2	L5	4116	C
2	L5	4122	G
2	L5	4127	A
2	L5	4141	G
2	L5	4142	C
2	L5	4143	G
2	L5	4144	C
2	L5	4146	G
2	L5	4162	C
2	L5	4163	U
2	L5	4164	C
2	L5	4170	A
2	L5	4183	G
2	L5	4184	G
2	L5	4191	G
2	L5	4203	A
2	L5	4212	A
2	L5	4220	6MZ
2	L5	4222	G
2	L5	4229	U
2	L5	4232	U
2	L5	4233	A

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Mol	Chain	Res	Type
2	L5	4234	A
2	L5	4251	A
2	L5	4254	G
2	L5	4257	A
2	L5	4258	C
2	L5	4265	U
2	L5	4268	A
2	L5	4273	A
2	L5	4281	A
2	L5	4291	G
2	L5	4295	U
2	L5	4304	A
2	L5	4305	G
2	L5	4314	C
2	L5	4319	C
2	L5	4329	G
2	L5	4330	G
2	L5	4332	C
2	L5	4339	A
2	L5	4349	C
2	L5	4350	C
2	L5	4354	U
2	L5	4373	G
2	L5	4377	G
2	L5	4378	A
2	L5	4379	A
2	L5	4387	C
2	L5	4391	G
2	L5	4394	A
2	L5	4421	C
2	L5	4422	A
2	L5	4448	G
2	L5	4449	A
2	L5	4464	A
2	L5	4466	C
2	L5	4475	G
2	L5	4488	A
2	L5	4500	PSU
2	L5	4512	U
2	L5	4513	A
2	L5	4519	C
2	L5	4524	G

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Mol	Chain	Res	Type
2	L5	4545	G
2	L5	4548	A
2	L5	4560	C
2	L5	4567	G
2	L5	4569	U
2	L5	4575	G
2	L5	4584	A
2	L5	4589	A
2	L5	4590	A2M
2	L5	4600	G
2	L5	4601	U
2	L5	4617	G
2	L5	4636	PSU
2	L5	4637	OMG
2	L5	4652	G
2	L5	4656	A
2	L5	4670	C
2	L5	4672	A
2	L5	4694	G
2	L5	4695	C
2	L5	4700	A
2	L5	4707	A
2	L5	4708	A
2	L5	4709	U
2	L5	4719	G
2	L5	4733	C
2	L5	4734	A
2	L5	4740	G
2	L5	4741	C
2	L5	4742	G
2	L5	4745	G
2	L5	4754	G
2	L5	4757	C
2	L5	4759	C
2	L5	4761	G
2	L5	4765	G
2	L5	4771	C
2	L5	4772	C
2	L5	4775	C
2	L5	4859	C
2	L5	4860	G
2	L5	4863	G

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Mol	Chain	Res	Type
2	L5	4870	G
2	L5	4871	C
2	L5	4875	G
2	L5	4877	G
2	L5	4881	U
2	L5	4882	U
2	L5	4883	C
2	L5	4889	G
2	L5	4895	C
2	L5	4896	G
2	L5	4897	G
2	L5	4899	G
2	L5	4900	C
2	L5	4901	G
2	L5	4909	A
2	L5	4910	G
2	L5	4912	G
2	L5	4914	C
2	L5	4925	U
2	L5	4927	G
2	L5	4928	C
2	L5	4934	A
2	L5	4937	C
2	L5	4940	C
2	L5	4941	G
2	L5	4943	A
2	L5	4944	C
2	L5	4947	U
2	L5	4955	A
2	L5	4960	G
2	L5	4976	U
2	L5	4979	A
2	L5	4988	U
2	L5	4989	U
2	L5	4991	U
2	L5	4995	U
2	L5	5007	A
2	L5	5013	C
2	L5	5014	A
2	L5	5017	G
2	L5	5020	G
2	L5	5022	U

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Mol	Chain	Res	Type
2	L5	5023	C
2	L5	5024	C
2	L5	5026	U
2	L5	5027	C
2	L5	5028	G
2	L5	5030	U
2	L5	5034	A
2	L5	5040	U
2	L5	5041	G
2	L5	5050	C
2	L5	5054	C
2	L5	5055	G
2	L5	5061	A
2	L5	5069	U
3	L7	7	G
3	L7	22	A
3	L7	33	U
3	L7	38	U
3	L7	53	U
3	L7	64	G
3	L7	100	A
3	L7	110	G
4	L8	23	C
4	L8	25	G
4	L8	34	U
4	L8	35	C
4	L8	38	U
4	L8	39	G
4	L8	59	A
4	L8	63	U
4	L8	80	A
4	L8	82	A
4	L8	84	A
4	L8	85	U
4	L8	87	G
4	L8	94	G
4	L8	103	A
4	L8	105	C
4	L8	111	U
4	L8	114	G
4	L8	124	U
4	L8	125	C

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Mol	Chain	Res	Type
4	L8	126	C
4	L8	127	U
4	L8	147	G
4	L8	150	C
4	L8	153	C
82	S2	4	C
82	S2	13	C
82	S2	14	C
82	S2	25	A
82	S2	33	G
82	S2	41	G
82	S2	44	U
82	S2	45	A
82	S2	46	A
82	S2	56	G
82	S2	58	C
82	S2	62	G
82	S2	65	C
82	S2	67	C
82	S2	68	A
82	S2	72	C
82	S2	73	C
82	S2	74	G
82	S2	76	U
82	S2	99	A2M
82	S2	103	A
82	S2	113	G
82	S2	114	G
82	S2	115	U
82	S2	126	G
82	S2	130	G
82	S2	143	U
82	S2	149	A
82	S2	155	G
82	S2	158	A
82	S2	160	U
82	S2	162	C
82	S2	170	A
82	S2	175	A
82	S2	187	G
82	S2	190	G
82	S2	191	A

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Mol	Chain	Res	Type
82	S2	196	C
82	S2	197	U
82	S2	198	U
82	S2	200	G
82	S2	203	G
82	S2	204	G
82	S2	206	G
82	S2	207	G
82	S2	208	G
82	S2	209	A
82	S2	213	G
82	S2	214	U
82	S2	220	U
82	S2	290	U
82	S2	291	G
82	S2	292	A
82	S2	295	C
82	S2	302	A
82	S2	306	C
82	S2	307	G
82	S2	308	G
82	S2	309	G
82	S2	312	G
82	S2	313	A
82	S2	314	U
82	S2	318	A
82	S2	319	C
82	S2	323	C
82	S2	324	C
82	S2	325	C
82	S2	326	C
82	S2	328	U
82	S2	329	G
82	S2	332	G
82	S2	339	A
82	S2	340	C
82	S2	347	G
82	S2	351	G
82	S2	360	A
82	S2	362	C
82	S2	364	A
82	S2	368	U

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Mol	Chain	Res	Type
82	S2	370	G
82	S2	383	G
82	S2	385	G
82	S2	386	C
82	S2	398	A
82	S2	407	G
82	S2	408	A
82	S2	409	C
82	S2	426	A
82	S2	428	OMU
82	S2	438	G
82	S2	448	A
82	S2	449	A
82	S2	450	C
82	S2	452	G
82	S2	459	C
82	S2	464	A
82	S2	465	A
82	S2	466	G
82	S2	471	G
82	S2	472	C
82	S2	473	A
82	S2	474	G
82	S2	476	A
82	S2	482	G
82	S2	487	U
82	S2	488	U
82	S2	492	C
82	S2	493	A
82	S2	500	A
82	S2	502	C
82	S2	517	OMC
82	S2	525	A
82	S2	531	A
82	S2	532	C
82	S2	536	A
82	S2	537	C
82	S2	540	U
82	S2	542	U
82	S2	544	G
82	S2	546	G
82	S2	547	G

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Mol	Chain	Res	Type
82	S2	557	U
82	S2	558	G
82	S2	559	G
82	S2	563	G
82	S2	564	A
82	S2	566	U
82	S2	576	A2M
82	S2	583	A
82	S2	587	A
82	S2	589	G
82	S2	590	A
82	S2	591	U
82	S2	593	C
82	S2	604	A
82	S2	614	C
82	S2	617	G
82	S2	628	A
82	S2	631	U
82	S2	643	A
82	S2	644	OMG
82	S2	655	A
82	S2	660	C
82	S2	664	A
82	S2	668	A2M
82	S2	669	A
82	S2	671	A
82	S2	672	A
82	S2	673	G
82	S2	688	U
82	S2	689	U
82	S2	692	G
82	S2	695	C
82	S2	696	G
82	S2	697	G
82	S2	698	G
82	S2	732	U
82	S2	733	C
82	S2	736	C
82	S2	737	G
82	S2	738	C
82	S2	749	U
82	S2	751	G

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Mol	Chain	Res	Type
82	S2	752	G
82	S2	753	C
82	S2	788	G
82	S2	791	C
82	S2	792	C
82	S2	797	C
82	S2	798	G
82	S2	799	OMU
82	S2	801	PSU
82	S2	821	G
82	S2	822	U
82	S2	823	U
82	S2	824	C
82	S2	827	A
82	S2	830	A
82	S2	834	C
82	S2	835	C
82	S2	836	G
82	S2	837	A
82	S2	838	G
82	S2	839	C
82	S2	842	C
82	S2	844	U
82	S2	847	A
82	S2	859	G
82	S2	867	OMG
82	S2	870	A
82	S2	871	U
82	S2	874	G
82	S2	878	G
82	S2	880	G
82	S2	888	U
82	S2	889	U
82	S2	891	G
82	S2	893	U
82	S2	896	U
82	S2	897	U
82	S2	898	U
82	S2	899	U
82	S2	900	C
82	S2	901	G
82	S2	903	A

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Mol	Chain	Res	Type
82	S2	904	A
82	S2	913	A
82	S2	920	A
82	S2	930	C
82	S2	933	G
82	S2	934	G
82	S2	939	U
82	S2	963	A
82	S2	970	G
82	S2	971	G
82	S2	972	A
82	S2	985	G
82	S2	990	A
82	S2	992	A
82	S2	997	A
82	S2	999	G
82	S2	1001	A
82	S2	1008	A
82	S2	1017	U
82	S2	1023	A
82	S2	1027	A
82	S2	1061	U
82	S2	1062	A
82	S2	1083	A
82	S2	1085	C
82	S2	1087	A
82	S2	1109	C
82	S2	1113	A
82	S2	1116	C
82	S2	1121	G
82	S2	1126	G
82	S2	1133	A
82	S2	1138	C
82	S2	1148	A
82	S2	1150	A
82	S2	1153	C
82	S2	1154	U
82	S2	1170	A
82	S2	1195	A
82	S2	1207	G
82	S2	1208	A
82	S2	1215	C

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Mol	Chain	Res	Type
82	S2	1216	C
82	S2	1217	A
82	S2	1220	A
82	S2	1224	G
82	S2	1227	G
82	S2	1242	U
82	S2	1243	U
82	S2	1251	A
82	S2	1253	A
82	S2	1256	G
82	S2	1257	G
82	S2	1264	C
82	S2	1271	C
82	S2	1272	OMC
82	S2	1274	G
82	S2	1275	G
82	S2	1281	G
82	S2	1283	C
82	S2	1288	OMU
82	S2	1294	G
82	S2	1295	A
82	S2	1301	A
82	S2	1302	G
82	S2	1303	C
82	S2	1308	U
82	S2	1309	C
82	S2	1342	U
82	S2	1357	A
82	S2	1358	U
82	S2	1371	U
82	S2	1372	U
82	S2	1376	A
82	S2	1378	A
82	S2	1382	A
82	S2	1396	A
82	S2	1402	A
82	S2	1413	G
82	S2	1418	C
82	S2	1419	C
82	S2	1420	G
82	S2	1421	A
82	S2	1422	G

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Mol	Chain	Res	Type
82	S2	1423	C
82	S2	1433	C
82	S2	1435	C
82	S2	1437	C
82	S2	1438	A
82	S2	1442	OMU
82	S2	1449	G
82	S2	1453	C
82	S2	1454	A
82	S2	1463	U
82	S2	1480	A
82	S2	1489	A
82	S2	1490	OMG
82	S2	1494	U
82	S2	1495	G
82	S2	1498	A
82	S2	1520	G
82	S2	1521	C
82	S2	1522	A
82	S2	1531	A
82	S2	1533	A
82	S2	1534	C
82	S2	1544	C
82	S2	1546	G
82	S2	1552	G
82	S2	1553	C
82	S2	1556	A
82	S2	1573	G
82	S2	1574	C
82	S2	1580	A
82	S2	1581	C
82	S2	1584	G
82	S2	1585	U
82	S2	1587	G
82	S2	1588	A
82	S2	1600	G
82	S2	1604	G
82	S2	1606	G
82	S2	1621	U
82	S2	1623	A
82	S2	1631	U
82	S2	1633	A

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Mol	Chain	Res	Type
82	S2	1634	A
82	S2	1637	A
82	S2	1638	G
82	S2	1648	G
82	S2	1649	U
82	S2	1654	G
82	S2	1663	A
82	S2	1665	G
82	S2	1683	C
82	S2	1686	G
82	S2	1695	A
82	S2	1698	C
82	S2	1699	A
82	S2	1715	A
82	S2	1721	U
82	S2	1722	G
82	S2	1744	G
82	S2	1745	A
82	S2	1752	C
82	S2	1753	C
82	S2	1754	G
82	S2	1755	C
82	S2	1757	G
82	S2	1759	G
82	S2	1761	U
82	S2	1772	C
82	S2	1773	C
82	S2	1774	C
82	S2	1777	G
82	S2	1783	C
82	S2	1784	G
82	S2	1786	U
82	S2	1798	C
82	S2	1810	U
82	S2	1821	U
82	S2	1825	A
82	S2	1826	G
82	S2	1831	A
82	S2	1835	A
82	S2	1838	U
82	S2	1849	G
82	S2	1851	MA6

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Mol	Chain	Res	Type
82	S2	1861	G
82	S2	1862	G
82	S2	1863	A
82	S2	1864	U
82	S2	1865	C
83	Zt	6	G
83	Zt	7	A
83	Zt	8	U
83	Zt	10	G
83	Zt	11	C
83	Zt	14	A
83	Zt	15	G
83	Zt	16	C
83	Zt	18	U
83	Zt	20	U
83	Zt	21	A
83	Zt	24	G
83	Zt	29	A
83	Zt	30	G
83	Zt	33	U
83	Zt	34	U
83	Zt	35	U
83	Zt	36	U
83	Zt	37	A
83	Zt	38	A
83	Zt	43	A
83	Zt	45	G
83	Zt	47	U
83	Zt	48	C
83	Zt	49	C
83	Zt	53	G
83	Zt	56	C
83	Zt	57	A
83	Zt	58	A
83	Zt	59	G
83	Zt	60	U
83	Zt	61	C
83	Zt	63	C
83	Zt	66	U
83	Zt	67	U
83	Zt	69	G
83	Zt	71	G

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Mol	Chain	Res	Type
83	Zt	72	C

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L5	406	C
2	L5	493	G
2	L5	914	U
2	L5	1082	C
2	L5	1633	G
2	L5	1703	C
2	L5	1977	C
2	L5	2416	G
2	L5	2675	G
2	L5	2760	G
2	L5	3673	C
2	L5	4600	G
2	L5	4699	U
2	L5	4913	G
82	S2	291	G
82	S2	563	G
82	S2	688	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

178 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PSU	L5	1582	2	18,21,22	1.11	2 (11%)	21,30,33	1.91	4 (19%)
4	PSU	L8	69	4	18,21,22	1.08	2 (11%)	21,30,33	2.00	6 (28%)
82	A2M	S2	668	85,82	22,25,26	1.29	2 (9%)	30,36,39	1.54	6 (20%)
82	A2M	S2	99	85,82	22,25,26	1.20	1 (4%)	30,36,39	1.59	7 (23%)
2	A2M	L5	1323	2	22,25,26	1.27	2 (9%)	30,36,39	1.59	9 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	L5	2876	2	23,26,27	0.56	0	32,38,41	0.51	0
82	A2M	S2	1383	82	22,25,26	1.13	1 (4%)	30,36,39	1.70	7 (23%)
2	A2M	L5	398	2	22,25,26	1.24	3 (13%)	30,36,39	1.65	8 (26%)
2	A2M	L5	400	2	22,25,26	1.27	3 (13%)	30,36,39	1.58	9 (30%)
2	A2M	L5	4571	2	22,25,26	1.25	2 (9%)	30,36,39	1.56	9 (30%)
2	OMG	L5	4618	2	23,26,27	0.58	0	32,38,41	0.52	0
2	PSU	L5	1677	2	18,21,22	1.04	2 (11%)	21,30,33	1.98	5 (23%)
2	OMC	L5	3808	2	19,22,23	0.67	0	25,31,34	0.85	2 (8%)
82	PSU	S2	1056	82	18,21,22	1.11	2 (11%)	21,30,33	2.05	5 (23%)
82	A2M	S2	27	82	22,25,26	1.18	1 (4%)	30,36,39	1.53	8 (26%)
82	4AC	S2	1337	82	21,24,25	0.40	0	28,34,37	0.70	1 (3%)
82	A2M	S2	166	82	22,25,26	1.27	2 (9%)	30,36,39	1.57	7 (23%)
82	MA6	S2	1850	82	23,26,27	1.29	2 (8%)	33,38,41	3.37	12 (36%)
82	B8N	S2	1248	82	25,29,30	3.24	6 (24%)	28,42,45	1.97	8 (28%)
2	PSU	L5	4442	2	18,21,22	1.11	3 (16%)	21,30,33	2.06	6 (28%)
82	OMU	S2	627	82	19,22,23	3.39	7 (36%)	25,31,34	1.81	5 (20%)
82	OMU	S2	116	82	19,22,23	3.31	7 (36%)	25,31,34	1.75	5 (20%)
82	PSU	S2	1232	82	18,21,22	1.07	1 (5%)	21,30,33	1.92	4 (19%)
2	PSU	L5	3695	2	18,21,22	1.02	1 (5%)	21,30,33	1.96	5 (23%)
2	OMU	L5	4620	2	19,22,23	3.15	7 (36%)	25,31,34	1.74	5 (20%)
2	OMC	L5	2365	85,2	19,22,23	0.64	0	25,31,34	0.62	0
82	OMU	S2	1288	82	19,22,23	3.38	7 (36%)	25,31,34	1.77	5 (20%)
82	PSU	S2	1367	82	18,21,22	1.09	1 (5%)	21,30,33	1.87	4 (19%)
82	OMG	S2	1328	82	23,26,27	0.51	0	32,38,41	0.48	0
2	PSU	L5	4972	2	18,21,22	1.00	1 (5%)	21,30,33	1.99	5 (23%)
2	UY1	L5	3818	2	19,22,23	4.81	8 (42%)	21,31,34	2.00	5 (23%)
2	PSU	L5	4521	85,2	18,21,22	1.06	2 (11%)	21,30,33	1.95	4 (19%)
2	OMG	L5	1316	2	23,26,27	0.60	0	32,38,41	0.53	0
2	PSU	L5	1781	2	18,21,22	1.06	1 (5%)	21,30,33	1.93	4 (19%)
2	A2M	L5	4590	2	22,25,26	1.18	2 (9%)	30,36,39	1.60	7 (23%)
2	PSU	L5	4673	85,2	18,21,22	1.02	2 (11%)	21,30,33	1.86	4 (19%)
82	PSU	S2	1046	82	18,21,22	1.12	2 (11%)	21,30,33	1.98	6 (28%)
2	PSU	L5	4299	2	18,21,22	1.01	1 (5%)	21,30,33	1.90	4 (19%)
2	OMG	L5	3627	2	23,26,27	0.56	0	32,38,41	0.60	0
2	PSU	L5	4296	2	18,21,22	1.06	1 (5%)	21,30,33	2.00	4 (19%)
2	OMC	L5	1340	2	19,22,23	0.68	0	25,31,34	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMC	L5	2824	2	19,22,23	0.68	0	25,31,34	0.76	1 (4%)
2	PSU	L5	4493	2	18,21,22	1.02	1 (5%)	21,30,33	1.78	4 (19%)
82	PSU	S2	93	82	18,21,22	1.10	1 (5%)	21,30,33	1.79	4 (19%)
2	UR3	L5	4530	2	19,22,23	2.65	7 (36%)	26,32,35	1.52	3 (11%)
82	OMC	S2	1391	82	19,22,23	0.57	0	25,31,34	0.85	1 (4%)
2	A2M	L5	1524	2	22,25,26	1.27	2 (9%)	30,36,39	1.56	9 (30%)
82	OMC	S2	1272	82	19,22,23	0.50	0	25,31,34	0.76	0
2	PSU	L5	2839	2	18,21,22	1.03	2 (11%)	21,30,33	1.81	4 (19%)
2	5MC	L5	3782	85,2	19,22,23	0.75	0	26,32,35	0.81	1 (3%)
82	OMG	S2	644	82	23,26,27	0.51	0	32,38,41	0.46	0
82	PSU	S2	1004	82	18,21,22	1.08	1 (5%)	21,30,33	1.96	4 (19%)
2	PSU	L5	1782	2	18,21,22	1.08	1 (5%)	21,30,33	1.94	4 (19%)
2	PSU	L5	4532	2	18,21,22	1.07	1 (5%)	21,30,33	1.96	4 (19%)
82	PSU	S2	109	82	18,21,22	1.09	2 (11%)	21,30,33	2.03	5 (23%)
2	PSU	L5	4628	2	18,21,22	1.06	2 (11%)	21,30,33	2.00	4 (19%)
2	PSU	L5	3637	2	18,21,22	1.03	1 (5%)	21,30,33	2.00	3 (14%)
2	OMG	L5	3899	2	23,26,27	0.59	0	32,38,41	0.52	0
2	6MZ	L5	4220	2	22,25,26	3.98	12 (54%)	29,36,39	2.50	11 (37%)
82	OMU	S2	121	82	19,22,23	3.35	7 (36%)	25,31,34	1.83	5 (20%)
2	OMG	L5	4494	2	23,26,27	0.60	0	32,38,41	0.53	0
82	OMC	S2	1703	82	19,22,23	0.59	0	25,31,34	0.61	0
2	OMC	L5	3841	2	19,22,23	0.68	0	25,31,34	0.59	0
2	A2M	L5	3830	2	22,25,26	1.19	1 (4%)	30,36,39	1.56	8 (26%)
2	A2M	L5	3825	2	22,25,26	1.20	2 (9%)	30,36,39	1.56	8 (26%)
2	PSU	L5	4353	2	18,21,22	1.09	2 (11%)	21,30,33	1.99	4 (19%)
82	OMG	S2	601	82	23,26,27	0.52	0	32,38,41	0.42	0
82	PSU	S2	686	82	18,21,22	1.05	1 (5%)	21,30,33	1.96	4 (19%)
2	OMC	L5	3701	2	19,22,23	0.70	0	25,31,34	1.71	4 (16%)
82	PSU	S2	406	82	18,21,22	1.08	1 (5%)	21,30,33	2.05	5 (23%)
2	PSU	L5	4471	2	18,21,22	1.06	2 (11%)	21,30,33	1.93	4 (19%)
2	OMG	L5	4228	2	23,26,27	0.57	0	32,38,41	0.58	0
82	PSU	S2	681	82	18,21,22	1.07	2 (11%)	21,30,33	1.93	4 (19%)
2	A2M	L5	2787	2	22,25,26	1.12	1 (4%)	30,36,39	1.49	8 (26%)
2	OMG	L5	4499	2	23,26,27	0.53	0	32,38,41	0.47	0
2	PSU	L5	3822	2	18,21,22	1.09	3 (16%)	21,30,33	2.07	6 (28%)
2	A2M	L5	3867	2	22,25,26	1.26	3 (13%)	30,36,39	1.57	8 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A2M	L5	3785	85,2	22,25,26	1.16	1 (4%)	30,36,39	1.61	9 (30%)
2	PSU	L5	3851	2	18,21,22	1.04	1 (5%)	21,30,33	1.92	4 (19%)
2	OMU	L5	4227	2	19,22,23	3.25	7 (36%)	25,31,34	1.90	5 (20%)
82	OMG	S2	867	82	23,26,27	0.54	0	32,38,41	0.53	0
2	PSU	L5	1536	2	18,21,22	1.06	1 (5%)	21,30,33	2.00	4 (19%)
82	PSU	S2	801	82	18,21,22	1.13	1 (5%)	21,30,33	1.91	4 (19%)
2	OMU	L5	2837	2	19,22,23	3.27	7 (36%)	25,31,34	1.84	5 (20%)
82	PSU	S2	1081	82	18,21,22	1.05	1 (5%)	21,30,33	1.98	5 (23%)
82	A2M	S2	576	82	22,25,26	1.20	1 (4%)	30,36,39	1.55	6 (20%)
2	PSU	L5	4579	2	18,21,22	1.04	1 (5%)	21,30,33	1.96	4 (19%)
2	OMC	L5	2351	85,2	19,22,23	0.70	0	25,31,34	1.23	2 (8%)
82	A2M	S2	1031	82	22,25,26	1.18	2 (9%)	30,36,39	1.57	8 (26%)
82	OMG	S2	509	82	23,26,27	0.52	0	32,38,41	0.46	0
82	6MZ	S2	1832	85,82	26,26,26	2.77	5 (19%)	36,39,39	2.08	10 (27%)
2	PSU	L5	1792	2	18,21,22	1.02	1 (5%)	21,30,33	1.91	4 (19%)
2	OMG	L5	4392	2	23,26,27	0.59	0	32,38,41	0.52	0
82	A2M	S2	484	82	22,25,26	1.19	1 (4%)	30,36,39	1.48	7 (23%)
82	PSU	S2	1244	82	18,21,22	1.05	1 (5%)	21,30,33	1.88	4 (19%)
82	PSU	S2	863	82	18,21,22	1.06	1 (5%)	21,30,33	1.92	4 (19%)
82	4AC	S2	1842	82	21,24,25	0.40	0	28,34,37	0.47	0
82	OMG	S2	683	82	23,26,27	0.54	0	32,38,41	0.47	0
82	PSU	S2	105	82	18,21,22	1.10	1 (5%)	21,30,33	1.92	4 (19%)
2	OMG	L5	1522	2	23,26,27	0.59	0	32,38,41	0.57	0
2	PSU	L5	5010	2	18,21,22	1.06	2 (11%)	21,30,33	1.93	4 (19%)
2	A2M	L5	1534	85,2	22,25,26	1.25	2 (9%)	30,36,39	1.47	7 (23%)
2	OMC	L5	3869	2	19,22,23	0.65	0	25,31,34	0.72	0
2	OMG	L5	3744	2	23,26,27	0.58	0	32,38,41	0.47	0
2	OMC	L5	2861	2	19,22,23	0.63	0	25,31,34	0.78	1 (4%)
2	OMU	L5	4306	2	19,22,23	3.22	7 (36%)	25,31,34	1.87	5 (20%)
2	PSU	L5	3884	2	18,21,22	1.05	2 (11%)	21,30,33	1.98	4 (19%)
82	OMU	S2	428	82	19,22,23	3.31	7 (36%)	25,31,34	1.89	5 (20%)
2	PSU	L5	4403	2	18,21,22	1.00	2 (11%)	21,30,33	2.04	6 (28%)
82	PSU	S2	1045	82	18,21,22	1.07	1 (5%)	21,30,33	1.89	4 (19%)
2	PSU	L5	1744	85,2	18,21,22	1.08	2 (11%)	21,30,33	1.91	6 (28%)
82	PSU	S2	1177	82	18,21,22	1.06	2 (11%)	21,30,33	1.89	4 (19%)
2	A2M	L5	2363	85,2	22,25,26	1.19	2 (9%)	30,36,39	1.54	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	L5	4370	2	23,26,27	0.59	0	32,38,41	0.53	0
2	OMG	L5	4637	2	23,26,27	0.58	0	32,38,41	0.49	0
2	OMG	L5	2424	2	23,26,27	0.55	0	32,38,41	0.48	0
2	PSU	L5	4361	2	18,21,22	1.03	1 (5%)	21,30,33	1.96	4 (19%)
82	A2M	S2	159	82	22,25,26	1.17	1 (4%)	30,36,39	1.56	9 (30%)
2	A2M	L5	2401	2	22,25,26	1.22	2 (9%)	30,36,39	1.61	7 (23%)
2	PSU	L5	1683	2	18,21,22	1.11	2 (11%)	21,30,33	1.96	4 (19%)
2	PSU	L5	2632	2	18,21,22	1.08	1 (5%)	21,30,33	1.88	4 (19%)
2	OMU	L5	3925	2	19,22,23	3.20	7 (36%)	25,31,34	1.89	5 (20%)
82	PSU	S2	866	82	18,21,22	1.07	1 (5%)	21,30,33	1.98	5 (23%)
2	OMC	L5	4456	2	19,22,23	0.74	1 (5%)	25,31,34	0.87	1 (4%)
82	OMU	S2	354	82	19,22,23	3.23	7 (36%)	25,31,34	1.88	5 (20%)
2	OMG	L5	1625	2	23,26,27	0.57	0	32,38,41	0.47	0
2	PSU	L5	4312	2	18,21,22	1.09	2 (11%)	21,30,33	1.93	4 (19%)
82	PSU	S2	966	82	18,21,22	1.09	2 (11%)	21,30,33	1.87	4 (19%)
82	MA6	S2	1851	82	23,26,27	1.30	2 (8%)	33,38,41	3.38	12 (36%)
82	PSU	S2	649	82	18,21,22	1.04	1 (5%)	21,30,33	1.94	4 (19%)
2	PSU	L5	5001	2	18,21,22	1.10	2 (11%)	21,30,33	1.91	4 (19%)
2	1MA	L5	1322	85,2	21,25,26	0.60	0	30,37,40	0.80	2 (6%)
2	PSU	L5	4431	2	18,21,22	1.07	2 (11%)	21,30,33	1.95	4 (19%)
82	OMU	S2	172	82	19,22,23	3.37	7 (36%)	25,31,34	1.83	4 (16%)
2	A2M	L5	1871	85,2	22,25,26	1.31	3 (13%)	30,36,39	1.63	8 (26%)
2	OMG	L5	3792	2	23,26,27	0.57	0	32,38,41	0.49	0
82	OMU	S2	1442	82	19,22,23	3.32	7 (36%)	25,31,34	1.81	4 (16%)
2	PSU	L5	4576	2	18,21,22	1.07	2 (11%)	21,30,33	1.94	4 (19%)
2	PSU	L5	1860	2	18,21,22	1.04	1 (5%)	21,30,33	1.82	4 (19%)
2	A2M	L5	4523	85,2	22,25,26	1.35	3 (13%)	30,36,39	1.60	7 (23%)
2	PSU	L5	3920	85,2	18,21,22	1.09	2 (11%)	21,30,33	2.02	5 (23%)
2	OMC	L5	4536	2	19,22,23	0.68	0	25,31,34	0.68	0
2	OMG	L5	4196	2,1	23,26,27	0.56	0	32,38,41	0.42	0
2	OMC	L5	2804	2	19,22,23	0.65	0	25,31,34	0.62	0
2	OMG	L5	4623	2	23,26,27	0.60	0	32,38,41	0.52	0
2	A2M	L5	3718	2	22,25,26	1.20	2 (9%)	30,36,39	1.57	5 (16%)
2	OMU	L5	4498	2	19,22,23	3.19	7 (36%)	25,31,34	1.82	5 (20%)
2	PSU	L5	4293	2	18,21,22	1.10	2 (11%)	21,30,33	2.12	4 (19%)
4	PSU	L8	55	4	18,21,22	1.02	2 (11%)	21,30,33	1.89	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
82	OMU	S2	799	82	19,22,23	3.37	7 (36%)	25,31,34	1.84	5 (20%)
2	PSU	L5	4457	2	18,21,22	1.12	3 (16%)	21,30,33	1.98	5 (23%)
2	A2M	L5	2815	2	22,25,26	1.19	2 (9%)	30,36,39	1.52	8 (26%)
82	OMC	S2	462	82	19,22,23	0.54	0	25,31,34	0.71	0
2	PSU	L5	4500	2	18,21,22	1.09	2 (11%)	21,30,33	2.08	5 (23%)
82	PSU	S2	1174	82	18,21,22	1.08	2 (11%)	21,30,33	1.98	4 (19%)
2	PSU	L5	3853	85,2	18,21,22	1.06	1 (5%)	21,30,33	1.90	4 (19%)
82	OMG	S2	436	82	23,26,27	0.54	0	32,38,41	0.56	0
2	PSU	L5	4973	2	18,21,22	1.06	2 (11%)	21,30,33	1.94	5 (23%)
82	PSU	S2	651	82	18,21,22	1.10	1 (5%)	21,30,33	2.01	5 (23%)
82	A2M	S2	468	82	22,25,26	1.22	1 (4%)	30,36,39	1.68	7 (23%)
2	A2M	L5	1326	2	22,25,26	1.20	2 (9%)	30,36,39	1.47	9 (30%)
2	PSU	L5	4636	2	18,21,22	1.13	2 (11%)	21,30,33	2.01	6 (28%)
2	PSU	L5	4689	2	18,21,22	1.04	2 (11%)	21,30,33	2.14	5 (23%)
2	OMC	L5	2422	85,2	19,22,23	0.62	0	25,31,34	0.81	1 (4%)
2	5MC	L5	4447	2	19,22,23	0.90	1 (5%)	26,32,35	0.72	0
82	OMG	S2	1490	82	23,26,27	0.59	0	32,38,41	0.51	0
2	PSU	L5	1862	2	18,21,22	1.02	1 (5%)	21,30,33	1.94	4 (19%)
2	OMG	L5	2364	85,2	23,26,27	0.57	0	32,38,41	0.47	0
2	PSU	L5	3639	2	18,21,22	1.06	2 (11%)	21,30,33	1.98	4 (19%)
82	PSU	S2	814	82	18,21,22	1.10	1 (5%)	21,30,33	1.87	4 (19%)
4	OMG	L8	75	4	23,26,27	0.55	0	32,38,41	0.49	0
2	PSU	L5	4552	2	18,21,22	1.02	2 (11%)	21,30,33	1.97	5 (23%)
82	OMU	S2	1326	82	19,22,23	3.29	7 (36%)	25,31,34	1.88	5 (20%)
82	G7M	S2	1639	82,1	23,26,27	2.63	9 (39%)	34,39,42	2.58	11 (32%)
82	OMC	S2	517	82	19,22,23	0.58	0	25,31,34	0.65	0
82	OMC	S2	174	82	19,22,23	0.57	0	25,31,34	0.65	0
2	OMC	L5	3887	2	19,22,23	0.60	0	25,31,34	0.74	0
2	PSU	L5	3844	2	18,21,22	1.09	2 (11%)	21,30,33	1.95	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	L5	1582	2	-	0/7/25/26	0/2/2/2
4	PSU	L8	69	4	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	A2M	S2	668	85,82	-	2/9/27/28	0/3/3/3
82	A2M	S2	99	85,82	-	2/9/27/28	0/3/3/3
2	A2M	L5	1323	2	-	2/9/27/28	0/3/3/3
2	OMG	L5	2876	2	-	2/9/27/28	0/3/3/3
82	A2M	S2	1383	82	-	0/9/27/28	0/3/3/3
2	A2M	L5	398	2	-	3/9/27/28	0/3/3/3
2	A2M	L5	400	2	-	1/9/27/28	0/3/3/3
2	A2M	L5	4571	2	-	0/9/27/28	0/3/3/3
2	OMG	L5	4618	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	1677	2	-	4/7/25/26	0/2/2/2
2	OMC	L5	3808	2	-	0/9/27/28	0/2/2/2
82	PSU	S2	1056	82	-	0/7/25/26	0/2/2/2
82	A2M	S2	27	82	-	1/9/27/28	0/3/3/3
82	4AC	S2	1337	82	-	1/11/29/30	0/2/2/2
82	A2M	S2	166	82	-	0/9/27/28	0/3/3/3
82	MA6	S2	1850	82	-	0/11/29/30	0/3/3/3
82	B8N	S2	1248	82	-	5/16/34/35	0/2/2/2
2	PSU	L5	4442	2	-	0/7/25/26	0/2/2/2
82	OMU	S2	627	82	-	0/9/27/28	0/2/2/2
82	OMU	S2	116	82	-	1/9/27/28	0/2/2/2
82	PSU	S2	1232	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	3695	2	-	0/7/25/26	0/2/2/2
2	OMU	L5	4620	2	-	1/9/27/28	0/2/2/2
2	OMC	L5	2365	85,2	-	1/9/27/28	0/2/2/2
82	OMU	S2	1288	82	-	3/9/27/28	0/2/2/2
82	PSU	S2	1367	82	-	0/7/25/26	0/2/2/2
82	OMG	S2	1328	82	-	1/9/27/28	0/3/3/3
2	PSU	L5	4972	2	-	0/7/25/26	0/2/2/2
2	UY1	L5	3818	2	-	3/9/27/28	0/2/2/2
2	PSU	L5	4521	85,2	-	0/7/25/26	0/2/2/2
2	OMG	L5	1316	2	-	1/9/27/28	0/3/3/3
2	PSU	L5	1781	2	-	2/7/25/26	0/2/2/2
2	A2M	L5	4590	2	-	4/9/27/28	0/3/3/3
2	PSU	L5	4673	85,2	-	0/7/25/26	0/2/2/2
82	PSU	S2	1046	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	4299	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	3627	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	4296	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	1340	2	-	1/9/27/28	0/2/2/2
2	OMC	L5	2824	2	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	L5	4493	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	93	82	-	0/7/25/26	0/2/2/2
2	UR3	L5	4530	2	-	0/7/25/26	0/2/2/2
82	OMC	S2	1391	82	-	0/9/27/28	0/2/2/2
2	A2M	L5	1524	2	-	2/9/27/28	0/3/3/3
82	OMC	S2	1272	82	-	2/9/27/28	0/2/2/2
2	PSU	L5	2839	2	-	0/7/25/26	0/2/2/2
2	5MC	L5	3782	85,2	-	0/7/25/26	0/2/2/2
82	OMG	S2	644	82	-	4/9/27/28	0/3/3/3
82	PSU	S2	1004	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	1782	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	4532	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	109	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	4628	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	3637	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	3899	2	-	2/9/27/28	0/3/3/3
2	6MZ	L5	4220	2	-	2/9/27/28	0/3/3/3
82	OMU	S2	121	82	-	0/9/27/28	0/2/2/2
2	OMG	L5	4494	2	-	1/9/27/28	0/3/3/3
82	OMC	S2	1703	82	-	1/9/27/28	0/2/2/2
2	OMC	L5	3841	2	-	0/9/27/28	0/2/2/2
2	A2M	L5	3830	2	-	0/9/27/28	0/3/3/3
2	A2M	L5	3825	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	4353	2	-	0/7/25/26	0/2/2/2
82	OMG	S2	601	82	-	1/9/27/28	0/3/3/3
82	PSU	S2	686	82	-	0/7/25/26	0/2/2/2
2	OMC	L5	3701	2	-	6/9/27/28	0/2/2/2
82	PSU	S2	406	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	4471	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	4228	2	-	1/9/27/28	0/3/3/3
82	PSU	S2	681	82	-	0/7/25/26	0/2/2/2
2	A2M	L5	2787	2	-	5/9/27/28	0/3/3/3
2	OMG	L5	4499	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	3822	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	3867	2	-	3/9/27/28	0/3/3/3
2	A2M	L5	3785	85,2	-	1/9/27/28	0/3/3/3
2	PSU	L5	3851	2	-	0/7/25/26	0/2/2/2
2	OMU	L5	4227	2	-	1/9/27/28	0/2/2/2
82	OMG	S2	867	82	-	2/9/27/28	0/3/3/3
2	PSU	L5	1536	2	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	PSU	S2	801	82	-	2/7/25/26	0/2/2/2
2	OMU	L5	2837	2	-	0/9/27/28	0/2/2/2
82	PSU	S2	1081	82	-	1/7/25/26	0/2/2/2
82	A2M	S2	576	82	-	4/9/27/28	0/3/3/3
2	PSU	L5	4579	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	2351	85,2	-	2/9/27/28	0/2/2/2
82	A2M	S2	1031	82	-	0/9/27/28	0/3/3/3
82	OMG	S2	509	82	-	0/9/27/28	0/3/3/3
82	6MZ	S2	1832	85,82	-	5/12/28/28	0/3/3/3
2	PSU	L5	1792	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	4392	2	-	0/9/27/28	0/3/3/3
82	A2M	S2	484	82	-	0/9/27/28	0/3/3/3
82	PSU	S2	1244	82	-	0/7/25/26	0/2/2/2
82	PSU	S2	863	82	-	0/7/25/26	0/2/2/2
82	4AC	S2	1842	82	-	0/11/29/30	0/2/2/2
82	OMG	S2	683	82	-	2/9/27/28	0/3/3/3
82	PSU	S2	105	82	-	0/7/25/26	0/2/2/2
2	OMG	L5	1522	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	5010	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	1534	85,2	-	1/9/27/28	0/3/3/3
2	OMC	L5	3869	2	-	0/9/27/28	0/2/2/2
2	OMG	L5	3744	2	-	0/9/27/28	0/3/3/3
2	OMC	L5	2861	2	-	1/9/27/28	0/2/2/2
2	OMU	L5	4306	2	-	1/9/27/28	0/2/2/2
2	PSU	L5	3884	2	-	0/7/25/26	0/2/2/2
82	OMU	S2	428	82	-	6/9/27/28	0/2/2/2
2	PSU	L5	4403	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	1045	82	-	2/7/25/26	0/2/2/2
2	PSU	L5	1744	85,2	-	0/7/25/26	0/2/2/2
82	PSU	S2	1177	82	-	0/7/25/26	0/2/2/2
2	A2M	L5	2363	85,2	-	0/9/27/28	0/3/3/3
2	OMG	L5	4370	2	-	1/9/27/28	0/3/3/3
2	OMG	L5	4637	2	-	3/9/27/28	0/3/3/3
2	OMG	L5	2424	2	-	0/9/27/28	0/3/3/3
2	PSU	L5	4361	2	-	0/7/25/26	0/2/2/2
82	A2M	S2	159	82	-	1/9/27/28	0/3/3/3
2	A2M	L5	2401	2	-	2/9/27/28	0/3/3/3
2	PSU	L5	1683	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	2632	2	-	2/7/25/26	0/2/2/2
2	OMU	L5	3925	2	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	PSU	S2	866	82	-	0/7/25/26	0/2/2/2
2	OMC	L5	4456	2	-	0/9/27/28	0/2/2/2
82	OMU	S2	354	82	-	0/9/27/28	0/2/2/2
2	OMG	L5	1625	2	-	2/9/27/28	0/3/3/3
2	PSU	L5	4312	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	966	82	-	0/7/25/26	0/2/2/2
82	MA6	S2	1851	82	-	1/11/29/30	0/3/3/3
82	PSU	S2	649	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	5001	2	-	0/7/25/26	0/2/2/2
2	1MA	L5	1322	85,2	-	2/7/25/26	0/3/3/3
2	PSU	L5	4431	2	-	0/7/25/26	0/2/2/2
82	OMU	S2	172	82	-	0/9/27/28	0/2/2/2
2	A2M	L5	1871	85,2	-	0/9/27/28	0/3/3/3
2	OMG	L5	3792	2	-	2/9/27/28	0/3/3/3
82	OMU	S2	1442	82	-	2/9/27/28	0/2/2/2
2	PSU	L5	4576	2	-	0/7/25/26	0/2/2/2
2	PSU	L5	1860	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	4523	85,2	-	0/9/27/28	0/3/3/3
2	PSU	L5	3920	85,2	-	0/7/25/26	0/2/2/2
2	OMC	L5	4536	2	-	0/9/27/28	0/2/2/2
2	OMG	L5	4196	2,1	-	1/9/27/28	0/3/3/3
2	OMC	L5	2804	2	-	0/9/27/28	0/2/2/2
2	OMG	L5	4623	2	-	2/9/27/28	0/3/3/3
2	A2M	L5	3718	2	-	0/9/27/28	0/3/3/3
2	OMU	L5	4498	2	-	0/9/27/28	0/2/2/2
2	PSU	L5	4293	2	-	0/7/25/26	0/2/2/2
4	PSU	L8	55	4	-	0/7/25/26	0/2/2/2
82	OMU	S2	799	82	-	2/9/27/28	0/2/2/2
2	PSU	L5	4457	2	-	0/7/25/26	0/2/2/2
2	A2M	L5	2815	2	-	1/9/27/28	0/3/3/3
82	OMC	S2	462	82	-	0/9/27/28	0/2/2/2
2	PSU	L5	4500	2	-	4/7/25/26	0/2/2/2
82	PSU	S2	1174	82	-	0/7/25/26	0/2/2/2
2	PSU	L5	3853	85,2	-	0/7/25/26	0/2/2/2
82	OMG	S2	436	82	-	0/9/27/28	0/3/3/3
2	PSU	L5	4973	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	651	82	-	0/7/25/26	0/2/2/2
82	A2M	S2	468	82	-	1/9/27/28	0/3/3/3
2	A2M	L5	1326	2	-	2/9/27/28	0/3/3/3
2	PSU	L5	4636	2	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	L5	4689	2	-	0/7/25/26	0/2/2/2
2	OMC	L5	2422	85,2	-	2/9/27/28	0/2/2/2
2	5MC	L5	4447	2	-	4/7/25/26	0/2/2/2
82	OMG	S2	1490	82	-	2/9/27/28	0/3/3/3
2	PSU	L5	1862	2	-	0/7/25/26	0/2/2/2
2	OMG	L5	2364	85,2	-	2/9/27/28	0/3/3/3
2	PSU	L5	3639	2	-	0/7/25/26	0/2/2/2
82	PSU	S2	814	82	-	0/7/25/26	0/2/2/2
4	OMG	L8	75	4	-	0/9/27/28	0/3/3/3
2	PSU	L5	4552	2	-	0/7/25/26	0/2/2/2
82	OMU	S2	1326	82	-	0/9/27/28	0/2/2/2
82	G7M	S2	1639	82,1	-	2/7/25/26	0/3/3/3
82	OMC	S2	517	82	-	2/9/27/28	0/2/2/2
82	OMC	S2	174	82	-	0/9/27/28	0/2/2/2
2	OMC	L5	3887	2	-	1/9/27/28	0/2/2/2
2	PSU	L5	3844	2	-	1/7/25/26	0/2/2/2

All (331) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	3818	UY1	C6-C5	12.48	1.49	1.35
82	S2	1832	6MZ	C6-N6	12.27	1.48	1.34
2	L5	4220	6MZ	C6-N6	12.06	1.48	1.34
2	L5	3818	UY1	C2-N1	11.65	1.51	1.36
82	S2	1288	OMU	C2-N1	8.65	1.52	1.38
82	S2	799	OMU	C2-N1	8.50	1.51	1.38
2	L5	4220	6MZ	C3'-C2'	-8.35	1.30	1.53
82	S2	172	OMU	C2-N1	8.34	1.51	1.38
82	S2	627	OMU	C2-N1	8.28	1.51	1.38
82	S2	1442	OMU	C2-N1	8.10	1.51	1.38
82	S2	121	OMU	C2-N1	8.06	1.51	1.38
82	S2	116	OMU	C2-N1	8.00	1.51	1.38
82	S2	1248	B8N	C4-N3	-7.92	1.26	1.40
82	S2	1326	OMU	C2-N1	7.92	1.50	1.38
82	S2	428	OMU	C2-N1	7.88	1.50	1.38
2	L5	4227	OMU	C2-N1	7.84	1.50	1.38
2	L5	4306	OMU	C2-N1	7.80	1.50	1.38
2	L5	2837	OMU	C2-N1	7.80	1.50	1.38
82	S2	354	OMU	C2-N1	7.76	1.50	1.38
82	S2	1248	B8N	C6-N1	7.75	1.55	1.36
2	L5	3925	OMU	C2-N1	7.73	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	4498	OMU	C2-N1	7.56	1.50	1.38
2	L5	3818	UY1	C2-N3	7.56	1.49	1.37
2	L5	4620	OMU	C2-N1	7.44	1.50	1.38
82	S2	627	OMU	C2-N3	6.99	1.50	1.38
82	S2	172	OMU	C2-N3	6.96	1.50	1.38
82	S2	116	OMU	C2-N3	6.94	1.50	1.38
82	S2	121	OMU	C2-N3	6.94	1.50	1.38
82	S2	1248	B8N	C4-C5	6.93	1.63	1.47
82	S2	428	OMU	C2-N3	6.87	1.49	1.38
82	S2	1442	OMU	C2-N3	6.83	1.49	1.38
82	S2	799	OMU	C2-N3	6.82	1.49	1.38
82	S2	1326	OMU	C2-N3	6.81	1.49	1.38
82	S2	1288	OMU	C2-N3	6.79	1.49	1.38
2	L5	2837	OMU	C2-N3	6.79	1.49	1.38
2	L5	4227	OMU	C2-N3	6.66	1.49	1.38
82	S2	354	OMU	C2-N3	6.59	1.49	1.38
2	L5	4306	OMU	C2-N3	6.55	1.49	1.38
2	L5	3925	OMU	C2-N3	6.53	1.49	1.38
2	L5	4498	OMU	C2-N3	6.47	1.49	1.38
2	L5	4620	OMU	C2-N3	6.42	1.49	1.38
82	S2	1639	G7M	C4-N3	6.41	1.48	1.34
2	L5	4530	UR3	C6-C5	6.25	1.49	1.35
2	L5	4530	UR3	C2-N1	5.93	1.46	1.38
82	S2	1248	B8N	C2-N1	5.91	1.56	1.39
82	S2	428	OMU	C6-C5	5.88	1.48	1.35
82	S2	121	OMU	C6-C5	5.84	1.48	1.35
82	S2	627	OMU	C6-C5	5.79	1.48	1.35
82	S2	799	OMU	C6-C5	5.78	1.48	1.35
82	S2	172	OMU	C6-C5	5.78	1.48	1.35
82	S2	1288	OMU	C6-C5	5.77	1.48	1.35
2	L5	3925	OMU	O4-C4	-5.73	1.13	1.24
82	S2	116	OMU	C6-C5	5.73	1.48	1.35
2	L5	4227	OMU	C6-C5	5.72	1.48	1.35
82	S2	1326	OMU	C6-C5	5.72	1.48	1.35
82	S2	1442	OMU	C6-C5	5.72	1.48	1.35
2	L5	2837	OMU	C6-C5	5.69	1.48	1.35
2	L5	4620	OMU	O4-C4	-5.66	1.13	1.24
2	L5	4530	UR3	C2-N3	5.62	1.50	1.39
2	L5	4306	OMU	C6-C5	5.59	1.48	1.35
82	S2	354	OMU	C6-C5	5.59	1.48	1.35
2	L5	4498	OMU	C6-C5	5.59	1.48	1.35
2	L5	4620	OMU	C6-C5	5.59	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	354	OMU	O4-C4	-5.58	1.13	1.24
2	L5	4306	OMU	O4-C4	-5.57	1.13	1.24
2	L5	3925	OMU	C6-C5	5.57	1.48	1.35
2	L5	4227	OMU	O4-C4	-5.54	1.13	1.24
2	L5	4498	OMU	O4-C4	-5.54	1.13	1.24
82	S2	116	OMU	O4-C4	-5.53	1.13	1.24
82	S2	121	OMU	O4-C4	-5.51	1.13	1.24
82	S2	1326	OMU	O4-C4	-5.50	1.13	1.24
82	S2	428	OMU	O4-C4	-5.50	1.13	1.24
82	S2	627	OMU	O4-C4	-5.50	1.13	1.24
82	S2	172	OMU	O4-C4	-5.48	1.13	1.24
2	L5	2837	OMU	O4-C4	-5.47	1.13	1.24
82	S2	1442	OMU	O4-C4	-5.45	1.13	1.24
82	S2	1288	OMU	O4-C4	-5.37	1.14	1.24
82	S2	799	OMU	O4-C4	-5.34	1.14	1.24
82	S2	1639	G7M	C2-N3	5.34	1.46	1.33
2	L5	3818	UY1	C6-N1	5.29	1.45	1.36
82	S2	1248	B8N	C6-C5	5.19	1.42	1.35
82	S2	1639	G7M	C2-N2	4.80	1.45	1.34
2	L5	4220	6MZ	O4'-C1'	-4.77	1.31	1.42
82	S2	1639	G7M	C5-N7	-4.74	1.33	1.39
2	L5	4220	6MZ	O4'-C4'	4.73	1.55	1.45
2	L5	4220	6MZ	C5'-C4'	-4.53	1.38	1.51
82	S2	627	OMU	C4-N3	4.47	1.46	1.38
82	S2	1442	OMU	C4-N3	4.36	1.46	1.38
2	L5	2837	OMU	C4-N3	4.36	1.46	1.38
82	S2	172	OMU	C4-N3	4.33	1.46	1.38
82	S2	1326	OMU	C4-N3	4.31	1.46	1.38
82	S2	121	OMU	C4-N3	4.29	1.46	1.38
82	S2	799	OMU	C4-N3	4.27	1.45	1.38
2	L5	3818	UY1	C4-N3	4.25	1.46	1.38
82	S2	116	OMU	C4-N3	4.24	1.45	1.38
82	S2	428	OMU	C4-N3	4.22	1.45	1.38
82	S2	1288	OMU	C4-N3	4.21	1.45	1.38
82	S2	354	OMU	C4-N3	4.14	1.45	1.38
2	L5	4227	OMU	C4-N3	4.09	1.45	1.38
2	L5	4306	OMU	C4-N3	4.02	1.45	1.38
2	L5	4498	OMU	C4-N3	4.00	1.45	1.38
2	L5	3925	OMU	C4-N3	3.90	1.45	1.38
2	L5	4620	OMU	C4-N3	3.85	1.45	1.38
82	S2	1639	G7M	C5-C6	3.81	1.53	1.43
2	L5	3818	UY1	O4-C4	-3.72	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	S2	801	PSU	C6-C5	3.71	1.39	1.35
2	L5	4220	6MZ	C5-C4	-3.60	1.32	1.39
82	S2	1248	B8N	C1'-C5	3.59	1.58	1.50
2	L5	1323	A2M	O5'-C5'	-3.56	1.33	1.44
2	L5	3825	A2M	O5'-C5'	-3.55	1.33	1.44
82	S2	93	PSU	C6-C5	3.53	1.39	1.35
2	L5	2815	A2M	O5'-C5'	-3.52	1.33	1.44
2	L5	3785	A2M	O5'-C5'	-3.50	1.34	1.44
82	S2	814	PSU	C6-C5	3.50	1.39	1.35
82	S2	99	A2M	O5'-C5'	-3.49	1.34	1.44
82	S2	668	A2M	O5'-C5'	-3.49	1.34	1.44
82	S2	105	PSU	C6-C5	3.48	1.39	1.35
82	S2	484	A2M	O5'-C5'	-3.48	1.34	1.44
82	S2	966	PSU	C6-C5	3.46	1.39	1.35
2	L5	2787	A2M	O5'-C5'	-3.45	1.34	1.44
2	L5	3867	A2M	O5'-C5'	-3.45	1.34	1.44
2	L5	4523	A2M	O5'-C5'	-3.44	1.34	1.44
2	L5	1524	A2M	O5'-C5'	-3.44	1.34	1.44
2	L5	400	A2M	O5'-C5'	-3.44	1.34	1.44
82	S2	576	A2M	O5'-C5'	-3.43	1.34	1.44
2	L5	3830	A2M	O5'-C5'	-3.43	1.34	1.44
2	L5	2401	A2M	O5'-C5'	-3.43	1.34	1.44
2	L5	1871	A2M	O5'-C5'	-3.42	1.34	1.44
82	S2	468	A2M	O5'-C5'	-3.42	1.34	1.44
82	S2	1367	PSU	C6-C5	3.42	1.39	1.35
82	S2	1031	A2M	O5'-C5'	-3.41	1.34	1.44
2	L5	1326	A2M	O5'-C5'	-3.41	1.34	1.44
2	L5	4636	PSU	C6-C5	3.41	1.39	1.35
2	L5	2363	A2M	O5'-C5'	-3.41	1.34	1.44
82	S2	651	PSU	C6-C5	3.40	1.39	1.35
82	S2	406	PSU	C6-C5	3.40	1.39	1.35
82	S2	1383	A2M	O5'-C5'	-3.40	1.34	1.44
82	S2	1244	PSU	C6-C5	3.40	1.39	1.35
2	L5	4220	6MZ	C5-N7	-3.39	1.32	1.39
2	L5	3718	A2M	O5'-C5'	-3.39	1.34	1.44
2	L5	4571	A2M	O5'-C5'	-3.36	1.34	1.44
82	S2	866	PSU	C6-C5	3.35	1.39	1.35
82	S2	1056	PSU	C6-C5	3.35	1.39	1.35
2	L5	1582	PSU	C6-C5	3.35	1.39	1.35
82	S2	863	PSU	C6-C5	3.33	1.39	1.35
2	L5	398	A2M	O5'-C5'	-3.32	1.34	1.44
2	L5	4590	A2M	O5'-C5'	-3.32	1.34	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	1782	PSU	C6-C5	3.31	1.39	1.35
82	S2	1046	PSU	C6-C5	3.31	1.39	1.35
82	S2	1232	PSU	C6-C5	3.29	1.38	1.35
82	S2	686	PSU	C6-C5	3.29	1.38	1.35
82	S2	1174	PSU	C6-C5	3.29	1.38	1.35
82	S2	27	A2M	O5'-C5'	-3.29	1.34	1.44
82	S2	166	A2M	O5'-C5'	-3.29	1.34	1.44
2	L5	2632	PSU	C6-C5	3.28	1.38	1.35
2	L5	1683	PSU	C6-C5	3.27	1.38	1.35
2	L5	5001	PSU	C6-C5	3.27	1.38	1.35
2	L5	4312	PSU	C6-C5	3.25	1.38	1.35
82	S2	1832	6MZ	C5-N7	-3.25	1.33	1.39
82	S2	1004	PSU	C6-C5	3.25	1.38	1.35
82	S2	1045	PSU	C6-C5	3.25	1.38	1.35
2	L5	4532	PSU	C6-C5	3.23	1.38	1.35
2	L5	4296	PSU	C6-C5	3.23	1.38	1.35
2	L5	1781	PSU	C6-C5	3.20	1.38	1.35
82	S2	109	PSU	C6-C5	3.20	1.38	1.35
2	L5	4353	PSU	C6-C5	3.20	1.38	1.35
82	S2	1177	PSU	C6-C5	3.20	1.38	1.35
2	L5	3818	UY1	O2-C2	-3.19	1.16	1.23
2	L5	3818	UY1	C1'-C5	3.19	1.57	1.50
82	S2	649	PSU	C6-C5	3.19	1.38	1.35
4	L8	69	PSU	C6-C5	3.18	1.38	1.35
2	L5	1534	A2M	O5'-C5'	-3.17	1.34	1.44
2	L5	5010	PSU	C6-C5	3.17	1.38	1.35
2	L5	1744	PSU	C6-C5	3.15	1.38	1.35
2	L5	4220	6MZ	C8-N9	-3.15	1.32	1.37
2	L5	4293	PSU	C6-C5	3.15	1.38	1.35
2	L5	4500	PSU	C6-C5	3.14	1.38	1.35
82	S2	1850	MA6	C6-N6	3.14	1.45	1.36
82	S2	681	PSU	C6-C5	3.13	1.38	1.35
82	S2	1832	6MZ	C5-C4	-3.13	1.33	1.39
2	L5	4431	PSU	C6-C5	3.13	1.38	1.35
2	L5	4471	PSU	C6-C5	3.12	1.38	1.35
82	S2	159	A2M	O5'-C5'	-3.12	1.35	1.44
2	L5	4579	PSU	C6-C5	3.11	1.38	1.35
2	L5	4973	PSU	C6-C5	3.10	1.38	1.35
2	L5	3844	PSU	C6-C5	3.10	1.38	1.35
2	L5	4442	PSU	C6-C5	3.09	1.38	1.35
2	L5	1862	PSU	C6-C5	3.07	1.38	1.35
2	L5	4457	PSU	C6-C5	3.05	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	4493	PSU	C6-C5	3.04	1.38	1.35
2	L5	3920	PSU	C6-C5	3.03	1.38	1.35
2	L5	4220	6MZ	C2'-C1'	3.02	1.63	1.53
82	S2	1851	MA6	C6-N6	3.02	1.45	1.36
2	L5	3851	PSU	C6-C5	3.02	1.38	1.35
2	L5	1860	PSU	C6-C5	3.01	1.38	1.35
82	S2	1081	PSU	C6-C5	3.01	1.38	1.35
2	L5	3853	PSU	C6-C5	3.00	1.38	1.35
2	L5	4299	PSU	C6-C5	3.00	1.38	1.35
2	L5	4521	PSU	C6-C5	2.99	1.38	1.35
2	L5	3822	PSU	C6-C5	2.98	1.38	1.35
2	L5	3637	PSU	C6-C5	2.98	1.38	1.35
4	L8	55	PSU	C6-C5	2.96	1.38	1.35
2	L5	1792	PSU	C6-C5	2.94	1.38	1.35
2	L5	4361	PSU	C6-C5	2.94	1.38	1.35
2	L5	4628	PSU	C6-C5	2.93	1.38	1.35
2	L5	1536	PSU	C6-C5	2.91	1.38	1.35
2	L5	3695	PSU	C6-C5	2.88	1.38	1.35
2	L5	4972	PSU	C6-C5	2.87	1.38	1.35
82	S2	428	OMU	C5-C4	2.87	1.49	1.43
2	L5	4576	PSU	C6-C5	2.86	1.38	1.35
82	S2	799	OMU	C5-C4	2.86	1.49	1.43
82	S2	627	OMU	C5-C4	2.85	1.49	1.43
2	L5	2839	PSU	C6-C5	2.81	1.38	1.35
2	L5	3639	PSU	C6-C5	2.80	1.38	1.35
2	L5	4673	PSU	C6-C5	2.80	1.38	1.35
2	L5	4530	UR3	O2-C2	-2.79	1.17	1.22
82	S2	1326	OMU	C5-C4	2.79	1.49	1.43
82	S2	1639	G7M	C2-N1	2.77	1.44	1.37
2	L5	4552	PSU	C6-C5	2.76	1.38	1.35
82	S2	1832	6MZ	C8-N9	-2.76	1.32	1.37
82	S2	121	OMU	C5-C4	2.76	1.49	1.43
82	S2	668	A2M	O4'-C4'	-2.74	1.38	1.45
82	S2	1288	OMU	C5-C4	2.74	1.49	1.43
82	S2	172	OMU	C5-C4	2.73	1.49	1.43
2	L5	4523	A2M	O4'-C4'	-2.72	1.39	1.45
2	L5	3884	PSU	C6-C5	2.71	1.38	1.35
82	S2	1442	OMU	C5-C4	2.70	1.49	1.43
82	S2	799	OMU	C6-N1	2.67	1.44	1.38
82	S2	1288	OMU	C6-N1	2.65	1.44	1.38
82	S2	627	OMU	C6-N1	2.65	1.44	1.38
82	S2	121	OMU	C6-N1	2.65	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	4220	6MZ	O3'-C3'	2.65	1.49	1.43
2	L5	4498	OMU	C5-C4	2.64	1.49	1.43
2	L5	1323	A2M	O4'-C4'	-2.63	1.39	1.45
2	L5	4227	OMU	C5-C4	2.63	1.49	1.43
82	S2	1442	OMU	C6-N1	2.62	1.44	1.38
82	S2	116	OMU	C5-C4	2.60	1.49	1.43
82	S2	1639	G7M	O6-C6	-2.56	1.18	1.23
2	L5	4306	OMU	C5-C4	2.55	1.49	1.43
82	S2	1851	MA6	C5-C4	-2.54	1.34	1.39
82	S2	354	OMU	C5-C4	2.54	1.49	1.43
82	S2	428	OMU	C6-N1	2.54	1.44	1.38
2	L5	2837	OMU	C6-N1	2.54	1.44	1.38
2	L5	4689	PSU	C6-C5	2.54	1.38	1.35
82	S2	172	OMU	C6-N1	2.53	1.44	1.38
2	L5	1524	A2M	O4'-C4'	-2.52	1.39	1.45
2	L5	2837	OMU	C5-C4	2.51	1.49	1.43
2	L5	4498	OMU	C6-N1	2.50	1.44	1.38
82	S2	116	OMU	C6-N1	2.50	1.44	1.38
2	L5	400	A2M	O4'-C4'	-2.47	1.39	1.45
82	S2	354	OMU	C6-N1	2.47	1.44	1.38
82	S2	1326	OMU	C6-N1	2.47	1.44	1.38
82	S2	1850	MA6	C5-C4	-2.46	1.34	1.39
82	S2	1639	G7M	C6-N1	2.46	1.43	1.38
2	L5	4227	OMU	C6-N1	2.45	1.43	1.38
2	L5	1677	PSU	C6-C5	2.45	1.38	1.35
2	L5	4530	UR3	C6-N1	2.44	1.43	1.38
2	L5	3925	OMU	C5-C4	2.43	1.49	1.43
2	L5	4220	6MZ	C6-N1	-2.43	1.31	1.35
2	L5	4306	OMU	C6-N1	2.41	1.43	1.38
82	S2	1639	G7M	C4-N9	-2.40	1.32	1.38
2	L5	4571	A2M	O4'-C4'	-2.39	1.39	1.45
82	S2	1832	6MZ	C6-N1	-2.37	1.31	1.35
2	L5	1326	A2M	O4'-C4'	-2.36	1.39	1.45
2	L5	4620	OMU	C5-C4	2.34	1.48	1.43
2	L5	1871	A2M	O4'-C4'	-2.34	1.39	1.45
2	L5	4403	PSU	C6-C5	2.34	1.37	1.35
2	L5	4689	PSU	C4-C5	-2.33	1.37	1.44
2	L5	4523	A2M	O3'-C3'	-2.33	1.37	1.43
2	L5	2815	A2M	O4'-C4'	-2.32	1.39	1.45
2	L5	4620	OMU	C6-N1	2.32	1.43	1.38
2	L5	3925	OMU	C6-N1	2.29	1.43	1.38
2	L5	1534	A2M	O4'-C4'	-2.27	1.39	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	1677	PSU	C4-C5	-2.26	1.38	1.44
2	L5	3844	PSU	C4-C5	-2.26	1.38	1.44
2	L5	3867	A2M	O4'-C4'	-2.26	1.40	1.45
2	L5	1871	A2M	O3'-C3'	-2.24	1.37	1.43
2	L5	2363	A2M	O4'-C4'	-2.24	1.40	1.45
2	L5	3639	PSU	C4-C5	-2.23	1.38	1.44
2	L5	4293	PSU	C4-C5	-2.23	1.38	1.44
2	L5	3884	PSU	C4-C5	-2.22	1.38	1.44
2	L5	4530	UR3	C5-C4	2.22	1.49	1.43
2	L5	4576	PSU	C4-C5	-2.20	1.38	1.44
2	L5	4457	PSU	C4-C5	-2.19	1.38	1.44
2	L5	4628	PSU	C4-C5	-2.18	1.38	1.44
2	L5	3920	PSU	C4-C5	-2.17	1.38	1.44
2	L5	3867	A2M	O3'-C3'	-2.16	1.37	1.43
2	L5	3825	A2M	O4'-C4'	-2.16	1.40	1.45
2	L5	4403	PSU	C4-C5	-2.15	1.38	1.44
2	L5	3822	PSU	O4'-C1'	-2.15	1.40	1.43
2	L5	398	A2M	O4'-C4'	-2.14	1.40	1.45
2	L5	4442	PSU	C4-C5	-2.14	1.38	1.44
2	L5	2839	PSU	C4-C5	-2.13	1.38	1.44
2	L5	3822	PSU	C4-C5	-2.13	1.38	1.44
2	L5	1683	PSU	C4-C5	-2.13	1.38	1.44
2	L5	4353	PSU	C4-C5	-2.12	1.38	1.44
2	L5	1582	PSU	C4-C5	-2.12	1.38	1.44
2	L5	4312	PSU	C4-C5	-2.12	1.38	1.44
2	L5	4521	PSU	C4-C5	-2.12	1.38	1.44
2	L5	400	A2M	O3'-C3'	-2.11	1.37	1.43
2	L5	4590	A2M	O4'-C4'	-2.11	1.40	1.45
82	S2	1046	PSU	C4-C5	-2.10	1.38	1.44
2	L5	4973	PSU	C4-C5	-2.10	1.38	1.44
2	L5	5001	PSU	C4-C5	-2.10	1.38	1.44
2	L5	4447	5MC	C5-C4	-2.10	1.42	1.44
82	S2	1174	PSU	C4-C5	-2.09	1.38	1.44
2	L5	4431	PSU	C4-C5	-2.09	1.38	1.44
2	L5	4500	PSU	C4-C5	-2.09	1.38	1.44
2	L5	4442	PSU	O4'-C1'	-2.09	1.41	1.43
2	L5	4552	PSU	C4-C5	-2.08	1.38	1.44
2	L5	2401	A2M	O4'-C4'	-2.07	1.40	1.45
2	L5	4530	UR3	C3U-N3	2.06	1.50	1.47
82	S2	1031	A2M	O4'-C4'	-2.05	1.40	1.45
2	L5	4456	OMC	C4-N3	-2.05	1.30	1.34
2	L5	4471	PSU	C4-C5	-2.05	1.38	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L5	4636	PSU	C4-C5	-2.04	1.38	1.44
2	L5	3718	A2M	O4'-C4'	-2.04	1.40	1.45
2	L5	1744	PSU	C4-C5	-2.04	1.38	1.44
2	L5	4673	PSU	C4-C5	-2.03	1.38	1.44
82	S2	1056	PSU	C4-C5	-2.03	1.38	1.44
82	S2	1177	PSU	C4-C5	-2.03	1.38	1.44
82	S2	109	PSU	C4-C5	-2.02	1.38	1.44
2	L5	4457	PSU	O4'-C1'	-2.02	1.41	1.43
82	S2	681	PSU	C4-C5	-2.02	1.38	1.44
2	L5	4220	6MZ	C4-N9	-2.01	1.33	1.37
2	L5	5010	PSU	C4-C5	-2.01	1.38	1.44
4	L8	69	PSU	C4-C5	-2.01	1.38	1.44
2	L5	398	A2M	O3'-C3'	-2.01	1.38	1.43
4	L8	55	PSU	C4-C5	-2.00	1.38	1.44
82	S2	166	A2M	O3'-C3'	-2.00	1.38	1.43
82	S2	966	PSU	C4-C5	-2.00	1.38	1.44

All (705) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1851	MA6	N1-C6-N6	-12.11	102.11	116.86
82	S2	1850	MA6	N1-C6-N6	-12.08	102.14	116.86
82	S2	1850	MA6	C5-C6-N6	8.17	138.26	125.33
82	S2	1851	MA6	C5-C6-N6	7.88	137.80	125.33
82	S2	1639	G7M	C1'-N9-C8	-7.46	101.56	126.74
82	S2	1639	G7M	C1'-N9-C4	7.42	148.41	126.49
2	L5	3925	OMU	C4-N3-C2	-5.97	119.20	126.61
82	S2	428	OMU	C4-N3-C2	-5.97	119.20	126.61
2	L5	4227	OMU	C4-N3-C2	-5.88	119.31	126.61
82	S2	1326	OMU	C4-N3-C2	-5.84	119.36	126.61
2	L5	4306	OMU	C4-N3-C2	-5.76	119.46	126.61
82	S2	354	OMU	C4-N3-C2	-5.70	119.53	126.61
2	L5	4498	OMU	C4-N3-C2	-5.69	119.54	126.61
2	L5	4220	6MZ	N1-C2-N3	-5.67	119.99	128.58
82	S2	1832	6MZ	N1-C2-N3	-5.67	120.01	128.58
82	S2	1851	MA6	N1-C2-N3	-5.66	120.02	128.58
82	S2	627	OMU	C4-N3-C2	-5.66	119.59	126.61
82	S2	1850	MA6	N1-C2-N3	-5.57	120.15	128.58
82	S2	172	OMU	C4-N3-C2	-5.53	119.74	126.61
82	S2	1442	OMU	C4-N3-C2	-5.53	119.74	126.61
82	S2	121	OMU	C4-N3-C2	-5.52	119.76	126.61
2	L5	2837	OMU	C4-N3-C2	-5.46	119.83	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4689	PSU	N1-C2-N3	5.46	120.93	115.17
82	S2	799	OMU	C4-N3-C2	-5.43	119.87	126.61
82	S2	1851	MA6	N9-C8-N7	-5.39	106.29	113.94
2	L5	4293	PSU	N1-C2-N3	5.38	120.84	115.17
2	L5	4293	PSU	C4-N3-C2	-5.30	119.07	126.37
82	S2	1248	B8N	C5-C4-N3	5.30	125.77	116.15
2	L5	3637	PSU	N1-C2-N3	5.29	120.75	115.17
2	L5	4636	PSU	C4-N3-C2	-5.27	119.11	126.37
2	L5	3701	OMC	C1'-N1-C2	5.26	130.07	118.44
82	S2	1850	MA6	N9-C8-N7	-5.25	106.48	113.94
82	S2	116	OMU	C4-N3-C2	-5.25	120.10	126.61
82	S2	406	PSU	N1-C2-N3	5.18	120.64	115.17
2	L5	4530	UR3	C4-N3-C2	-5.17	120.42	124.58
2	L5	1536	PSU	N1-C2-N3	5.16	120.61	115.17
82	S2	1288	OMU	C4-N3-C2	-5.16	120.21	126.61
82	S2	1056	PSU	N1-C2-N3	5.15	120.60	115.17
2	L5	4500	PSU	N1-C2-N3	5.14	120.59	115.17
82	S2	1056	PSU	C4-N3-C2	-5.13	119.30	126.37
2	L5	3637	PSU	C4-N3-C2	-5.13	119.31	126.37
82	S2	406	PSU	C4-N3-C2	-5.11	119.34	126.37
82	S2	1081	PSU	C4-N3-C2	-5.11	119.34	126.37
2	L5	4403	PSU	C4-N3-C2	-5.10	119.34	126.37
2	L5	3695	PSU	C4-N3-C2	-5.10	119.34	126.37
2	L5	4457	PSU	C4-N3-C2	-5.10	119.35	126.37
2	L5	1677	PSU	C4-N3-C2	-5.09	119.36	126.37
82	S2	109	PSU	C4-N3-C2	-5.09	119.36	126.37
2	L5	4296	PSU	C4-N3-C2	-5.09	119.36	126.37
2	L5	4620	OMU	C4-N3-C2	-5.08	120.30	126.61
2	L5	1862	PSU	C4-N3-C2	-5.08	119.37	126.37
2	L5	1782	PSU	C4-N3-C2	-5.08	119.37	126.37
2	L5	3920	PSU	N1-C2-N3	5.08	120.53	115.17
82	S2	651	PSU	N1-C2-N3	5.07	120.52	115.17
4	L8	69	PSU	N1-C2-N3	5.07	120.51	115.17
2	L5	4299	PSU	C4-N3-C2	-5.07	119.39	126.37
2	L5	4442	PSU	C4-N3-C2	-5.07	119.39	126.37
2	L5	4521	PSU	C4-N3-C2	-5.05	119.42	126.37
82	S2	109	PSU	N1-C2-N3	5.04	120.48	115.17
2	L5	4442	PSU	N1-C2-N3	5.03	120.48	115.17
82	S2	863	PSU	C4-N3-C2	-5.03	119.45	126.37
82	S2	1174	PSU	C4-N3-C2	-5.03	119.45	126.37
2	L5	4628	PSU	C4-N3-C2	-5.02	119.45	126.37
2	L5	4361	PSU	C4-N3-C2	-5.02	119.46	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3920	PSU	C4-N3-C2	-5.01	119.47	126.37
2	L5	4689	PSU	C4-N3-C2	-5.01	119.47	126.37
2	L5	4361	PSU	N1-C2-N3	5.01	120.45	115.17
82	S2	686	PSU	C4-N3-C2	-5.00	119.48	126.37
2	L5	4296	PSU	N1-C2-N3	5.00	120.45	115.17
82	S2	866	PSU	C4-N3-C2	-5.00	119.48	126.37
2	L5	4353	PSU	C4-N3-C2	-5.00	119.48	126.37
2	L5	3822	PSU	N1-C2-N3	5.00	120.44	115.17
2	L5	4353	PSU	N1-C2-N3	5.00	120.44	115.17
2	L5	1781	PSU	N1-C2-N3	4.99	120.43	115.17
2	L5	4500	PSU	C4-N3-C2	-4.99	119.50	126.37
82	S2	105	PSU	N1-C2-N3	4.99	120.43	115.17
2	L5	4628	PSU	N1-C2-N3	4.98	120.42	115.17
2	L5	4552	PSU	C4-N3-C2	-4.98	119.51	126.37
4	L8	55	PSU	C4-N3-C2	-4.97	119.52	126.37
2	L5	3884	PSU	N1-C2-N3	4.97	120.41	115.17
82	S2	649	PSU	C4-N3-C2	-4.97	119.52	126.37
2	L5	4579	PSU	C4-N3-C2	-4.97	119.52	126.37
2	L5	4532	PSU	C4-N3-C2	-4.97	119.53	126.37
82	S2	1081	PSU	N1-C2-N3	4.97	120.41	115.17
2	L5	4431	PSU	C4-N3-C2	-4.97	119.53	126.37
2	L5	4673	PSU	C4-N3-C2	-4.96	119.54	126.37
82	S2	866	PSU	N1-C2-N3	4.96	120.40	115.17
2	L5	4579	PSU	N1-C2-N3	4.96	120.40	115.17
2	L5	4972	PSU	N1-C2-N3	4.95	120.39	115.17
82	S2	801	PSU	N1-C2-N3	4.95	120.39	115.17
2	L5	4457	PSU	N1-C2-N3	4.95	120.39	115.17
2	L5	3818	UY1	C4-N3-C2	-4.95	119.55	126.37
2	L5	3639	PSU	N1-C2-N3	4.95	120.39	115.17
2	L5	4972	PSU	C4-N3-C2	-4.95	119.56	126.37
2	L5	4532	PSU	N1-C2-N3	4.94	120.38	115.17
82	S2	1046	PSU	N1-C2-N3	4.94	120.38	115.17
2	L5	4403	PSU	N1-C2-N3	4.94	120.38	115.17
82	S2	1045	PSU	C4-N3-C2	-4.93	119.58	126.37
82	S2	686	PSU	N1-C2-N3	4.93	120.37	115.17
82	S2	651	PSU	C4-N3-C2	-4.93	119.59	126.37
2	L5	3822	PSU	C4-N3-C2	-4.92	119.59	126.37
82	S2	649	PSU	N1-C2-N3	4.92	120.36	115.17
2	L5	4220	6MZ	N9-C8-N7	-4.92	106.95	113.94
82	S2	1004	PSU	N1-C2-N3	4.90	120.34	115.17
82	S2	1174	PSU	N1-C2-N3	4.89	120.33	115.17
2	L5	4636	PSU	N1-C2-N3	4.89	120.32	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3884	PSU	C4-N3-C2	-4.88	119.64	126.37
2	L5	1677	PSU	N1-C2-N3	4.88	120.32	115.17
2	L5	3851	PSU	C4-N3-C2	-4.87	119.66	126.37
2	L5	4471	PSU	N1-C2-N3	4.87	120.31	115.17
2	L5	5010	PSU	N1-C2-N3	4.87	120.30	115.17
2	L5	3639	PSU	C4-N3-C2	-4.87	119.67	126.37
2	L5	4973	PSU	C4-N3-C2	-4.86	119.67	126.37
2	L5	4552	PSU	N1-C2-N3	4.86	120.30	115.17
2	L5	1792	PSU	C4-N3-C2	-4.86	119.68	126.37
2	L5	4431	PSU	N1-C2-N3	4.86	120.29	115.17
82	S2	1832	6MZ	C5-C4-N3	-4.86	120.03	126.72
2	L5	1792	PSU	N1-C2-N3	4.85	120.29	115.17
2	L5	3844	PSU	N1-C2-N3	4.85	120.28	115.17
2	L5	1582	PSU	N1-C2-N3	4.85	120.28	115.17
82	S2	681	PSU	N1-C2-N3	4.84	120.28	115.17
2	L5	4576	PSU	C4-N3-C2	-4.84	119.71	126.37
2	L5	1683	PSU	N1-C2-N3	4.84	120.27	115.17
2	L5	4576	PSU	N1-C2-N3	4.84	120.27	115.17
82	S2	1232	PSU	C4-N3-C2	-4.83	119.72	126.37
2	L5	3851	PSU	N1-C2-N3	4.83	120.26	115.17
4	L8	69	PSU	C4-N3-C2	-4.83	119.72	126.37
82	S2	1244	PSU	C4-N3-C2	-4.82	119.72	126.37
2	L5	4471	PSU	C4-N3-C2	-4.82	119.73	126.37
2	L5	1536	PSU	C4-N3-C2	-4.82	119.73	126.37
2	L5	1582	PSU	C4-N3-C2	-4.82	119.74	126.37
2	L5	1862	PSU	N1-C2-N3	4.82	120.25	115.17
82	S2	1004	PSU	C4-N3-C2	-4.81	119.74	126.37
82	S2	1177	PSU	C4-N3-C2	-4.81	119.74	126.37
2	L5	4312	PSU	N1-C2-N3	4.81	120.24	115.17
2	L5	4973	PSU	N1-C2-N3	4.81	120.24	115.17
2	L5	1782	PSU	N1-C2-N3	4.80	120.24	115.17
2	L5	4312	PSU	C4-N3-C2	-4.80	119.76	126.37
2	L5	3695	PSU	N1-C2-N3	4.80	120.23	115.17
82	S2	1232	PSU	N1-C2-N3	4.79	120.22	115.17
82	S2	1046	PSU	C4-N3-C2	-4.79	119.77	126.37
2	L5	2632	PSU	N1-C2-N3	4.79	120.22	115.17
2	L5	5001	PSU	C4-N3-C2	-4.79	119.77	126.37
82	S2	681	PSU	C4-N3-C2	-4.79	119.77	126.37
2	L5	3844	PSU	C4-N3-C2	-4.79	119.77	126.37
2	L5	1781	PSU	C4-N3-C2	-4.78	119.78	126.37
2	L5	1860	PSU	C4-N3-C2	-4.78	119.78	126.37
2	L5	1744	PSU	N1-C2-N3	4.78	120.21	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	863	PSU	N1-C2-N3	4.78	120.21	115.17
2	L5	4521	PSU	N1-C2-N3	4.77	120.20	115.17
2	L5	2632	PSU	C4-N3-C2	-4.77	119.81	126.37
2	L5	5001	PSU	N1-C2-N3	4.75	120.18	115.17
2	L5	4299	PSU	N1-C2-N3	4.74	120.17	115.17
2	L5	3853	PSU	C4-N3-C2	-4.74	119.84	126.37
2	L5	3853	PSU	N1-C2-N3	4.74	120.16	115.17
2	L5	5010	PSU	C4-N3-C2	-4.73	119.85	126.37
82	S2	1177	PSU	N1-C2-N3	4.72	120.15	115.17
82	S2	1244	PSU	N1-C2-N3	4.72	120.14	115.17
82	S2	105	PSU	C4-N3-C2	-4.72	119.88	126.37
2	L5	1683	PSU	C4-N3-C2	-4.71	119.89	126.37
2	L5	4493	PSU	C4-N3-C2	-4.70	119.89	126.37
82	S2	1248	B8N	C4-N3-C2	-4.70	119.83	125.62
82	S2	1045	PSU	N1-C2-N3	4.70	120.13	115.17
82	S2	814	PSU	N1-C2-N3	4.70	120.12	115.17
2	L5	2839	PSU	C4-N3-C2	-4.70	119.90	126.37
4	L8	55	PSU	N1-C2-N3	4.69	120.12	115.17
82	S2	1367	PSU	C4-N3-C2	-4.68	119.93	126.37
82	S2	814	PSU	C4-N3-C2	-4.67	119.94	126.37
82	S2	966	PSU	N1-C2-N3	4.65	120.07	115.17
2	L5	1744	PSU	C4-N3-C2	-4.64	119.97	126.37
82	S2	1383	A2M	C3'-C2'-C1'	-4.64	93.92	102.81
82	S2	1367	PSU	N1-C2-N3	4.64	120.06	115.17
82	S2	801	PSU	C4-N3-C2	-4.64	119.98	126.37
2	L5	4220	6MZ	C9-N6-C6	-4.63	118.55	122.85
82	S2	966	PSU	C4-N3-C2	-4.63	120.00	126.37
82	S2	1832	6MZ	N9-C8-N7	-4.61	107.39	113.94
2	L5	4220	6MZ	C5-C4-N3	-4.58	120.41	126.72
2	L5	4673	PSU	N1-C2-N3	4.57	119.99	115.17
2	L5	1860	PSU	N1-C2-N3	4.55	119.97	115.17
82	S2	93	PSU	C4-N3-C2	-4.55	120.10	126.37
82	S2	93	PSU	N1-C2-N3	4.55	119.96	115.17
2	L5	2839	PSU	N1-C2-N3	4.46	119.88	115.17
2	L5	4493	PSU	N1-C2-N3	4.46	119.88	115.17
82	S2	1851	MA6	C5-C4-N3	-4.42	120.64	126.72
82	S2	1639	G7M	C2-N3-C4	4.40	119.88	112.30
82	S2	1850	MA6	C5-C4-N3	-4.38	120.69	126.72
2	L5	3818	UY1	N1-C2-N3	4.36	119.77	115.17
82	S2	1851	MA6	C4-N9-C8	4.34	110.29	105.74
2	L5	4227	OMU	N3-C2-N1	4.32	120.52	114.89
2	L5	3701	OMC	C1'-N1-C6	-4.29	111.61	120.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	121	OMU	N3-C2-N1	4.11	120.24	114.89
82	S2	428	OMU	N3-C2-N1	4.04	120.14	114.89
2	L5	1871	A2M	C3'-C2'-C1'	-4.02	95.10	102.81
82	S2	1639	G7M	C5-C6-N1	4.02	120.15	111.84
2	L5	4306	OMU	N3-C2-N1	4.01	120.11	114.89
82	S2	354	OMU	N3-C2-N1	4.00	120.10	114.89
2	L5	4523	A2M	C3'-C2'-C1'	-3.99	95.16	102.81
2	L5	4498	OMU	N3-C2-N1	3.97	120.05	114.89
82	S2	799	OMU	N3-C2-N1	3.96	120.05	114.89
2	L5	3830	A2M	C3'-C2'-C1'	-3.96	95.22	102.81
82	S2	1850	MA6	C4-N9-C8	3.95	109.88	105.74
82	S2	99	A2M	C3'-C2'-C1'	-3.95	95.25	102.81
2	L5	2837	OMU	N3-C2-N1	3.93	120.01	114.89
2	L5	3925	OMU	C5-C4-N3	3.91	120.28	114.80
2	L5	2351	OMC	C1'-N1-C2	3.87	126.99	118.44
2	L5	398	A2M	C3'-C2'-C1'	-3.87	95.40	102.81
2	L5	3925	OMU	N3-C2-N1	3.85	119.90	114.89
82	S2	172	OMU	N3-C2-N1	3.80	119.84	114.89
2	L5	4620	OMU	N3-C2-N1	3.77	119.80	114.89
82	S2	1326	OMU	C5-C4-N3	3.77	120.07	114.80
82	S2	1326	OMU	N3-C2-N1	3.76	119.79	114.89
82	S2	627	OMU	C5-C4-N3	3.75	120.06	114.80
82	S2	1288	OMU	N3-C2-N1	3.75	119.77	114.89
82	S2	428	OMU	C5-C4-N3	3.74	120.04	114.80
82	S2	1442	OMU	C5-C4-N3	3.73	120.02	114.80
82	S2	1639	G7M	C5-C4-N3	-3.71	121.13	128.15
82	S2	116	OMU	N3-C2-N1	3.71	119.73	114.89
82	S2	576	A2M	O3'-C3'-C2'	3.71	121.57	111.19
2	L5	4498	OMU	C5-C4-N3	3.69	119.97	114.80
82	S2	354	OMU	C5-C4-N3	3.68	119.95	114.80
82	S2	1442	OMU	N3-C2-N1	3.68	119.68	114.89
82	S2	468	A2M	C3'-C2'-C1'	-3.67	95.79	102.81
2	L5	4306	OMU	C5-C4-N3	3.65	119.92	114.80
82	S2	576	A2M	C3'-C2'-C1'	-3.63	95.85	102.81
2	L5	2401	A2M	C3'-C2'-C1'	-3.63	95.86	102.81
82	S2	627	OMU	N3-C2-N1	3.61	119.59	114.89
82	S2	468	A2M	O3'-C3'-C2'	3.61	121.28	111.19
82	S2	1383	A2M	O3'-C3'-C2'	3.59	121.23	111.19
82	S2	1850	MA6	C2-N1-C6	3.57	120.56	111.83
82	S2	1850	MA6	C4-C5-C6	3.54	119.57	115.91
2	L5	4227	OMU	C5-C4-N3	3.53	119.75	114.80
82	S2	799	OMU	C5-C4-N3	3.51	119.72	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4689	PSU	C6-N1-C2	-3.50	119.44	122.69
82	S2	121	OMU	C5-C4-N3	3.49	119.69	114.80
2	L5	1683	PSU	O2-C2-N1	-3.49	119.19	122.79
2	L5	398	A2M	O3'-C3'-C2'	3.48	120.93	111.19
82	S2	1832	6MZ	C2-N3-C4	3.46	120.27	111.83
2	L5	1536	PSU	O2-C2-N1	-3.45	119.23	122.79
82	S2	172	OMU	C5-C4-N3	3.45	119.63	114.80
82	S2	1851	MA6	C2-N1-C6	3.45	120.25	111.83
2	L5	2837	OMU	C5-C4-N3	3.45	119.63	114.80
82	S2	1639	G7M	CN7-N7-C5	3.44	131.09	126.80
2	L5	1534	A2M	C3'-C2'-C1'	-3.44	96.22	102.81
2	L5	1524	A2M	O3'-C3'-C2'	3.43	120.78	111.19
82	S2	116	OMU	C5-C4-N3	3.43	119.60	114.80
2	L5	4689	PSU	O2-C2-N1	-3.42	119.26	122.79
2	L5	3718	A2M	C3'-C2'-C1'	-3.40	96.30	102.81
2	L5	4220	6MZ	C2-N3-C4	3.40	120.13	111.83
2	L5	4500	PSU	O2-C2-N1	-3.39	119.29	122.79
2	L5	1323	A2M	C2'-C1'-N9	3.39	119.33	113.75
82	S2	1248	B8N	N3-C2-N1	3.38	120.84	116.72
2	L5	4620	OMU	C5-C4-N3	3.37	119.52	114.80
82	S2	1851	MA6	N3-C4-N9	3.37	132.89	127.17
82	S2	1639	G7M	O6-C6-C5	-3.35	120.53	128.01
82	S2	1851	MA6	C4-C5-C6	3.35	119.38	115.91
82	S2	1248	B8N	C1'-C5-C4	3.34	122.67	117.61
82	S2	1832	6MZ	N3-C4-N9	3.33	132.83	127.17
82	S2	159	A2M	O3'-C3'-C2'	3.31	120.44	111.19
2	L5	4220	6MZ	C4-N9-C8	3.30	109.20	105.74
82	S2	1288	OMU	C5-C4-N3	3.30	119.42	114.80
2	L5	3818	UY1	C6-C5-C4	3.27	120.38	118.17
2	L5	4530	UR3	C5-C4-N3	3.25	119.32	115.04
2	L5	4590	A2M	C3'-C2'-C1'	-3.24	96.60	102.81
82	S2	99	A2M	O3'-C3'-C2'	3.23	120.23	111.19
2	L5	1871	A2M	C4-N9-C1'	-3.23	119.07	126.63
2	L5	2401	A2M	O3'-C3'-C2'	3.20	120.15	111.19
82	S2	1851	MA6	C2-N3-C4	3.19	119.63	111.83
82	S2	468	A2M	C4-N9-C1'	-3.19	119.17	126.63
2	L5	2787	A2M	O3'-C3'-C2'	3.18	120.08	111.19
2	L5	3853	PSU	O2-C2-N1	-3.16	119.53	122.79
2	L5	4972	PSU	O2-C2-N1	-3.15	119.54	122.79
2	L5	4552	PSU	O2-C2-N1	-3.15	119.54	122.79
2	L5	2837	OMU	O4-C4-C5	-3.14	119.75	125.16
82	S2	166	A2M	C3'-C2'-C1'	-3.14	96.80	102.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4571	A2M	C2'-C1'-N9	3.13	118.90	113.75
82	S2	1442	OMU	O4-C4-C5	-3.13	119.77	125.16
2	L5	3825	A2M	C3'-C2'-C1'	-3.13	96.82	102.81
82	S2	1850	MA6	C5-N7-C8	3.13	108.36	103.45
2	L5	4293	PSU	O2-C2-N1	-3.12	119.57	122.79
82	S2	1004	PSU	O2-C2-N1	-3.12	119.57	122.79
82	S2	1850	MA6	C2-N3-C4	3.11	119.43	111.83
82	S2	406	PSU	O2-C2-N1	-3.11	119.58	122.79
82	S2	354	OMU	O4-C4-C5	-3.11	119.81	125.16
82	S2	1850	MA6	N3-C4-N9	3.10	132.44	127.17
82	S2	27	A2M	O3'-C3'-C2'	3.10	119.86	111.19
2	L5	4628	PSU	O2-C2-N1	-3.10	119.60	122.79
82	S2	1031	A2M	C3'-C2'-C1'	-3.09	96.88	102.81
82	S2	1851	MA6	C5-N7-C8	3.09	108.31	103.45
82	S2	109	PSU	O2-C2-N1	-3.09	119.60	122.79
82	S2	801	PSU	O2-C2-N1	-3.09	119.60	122.79
2	L5	3925	OMU	O4-C4-C5	-3.09	119.84	125.16
2	L5	4403	PSU	O2-C2-N1	-3.09	119.61	122.79
2	L5	2401	A2M	C4-N9-C1'	-3.08	119.42	126.63
82	S2	1326	OMU	O4-C4-C5	-3.07	119.86	125.16
2	L5	4220	6MZ	C5-N7-C8	3.07	108.28	103.45
2	L5	3718	A2M	O3'-C3'-C2'	3.07	119.77	111.19
82	S2	1383	A2M	C4-N9-C1'	-3.06	119.46	126.63
2	L5	5010	PSU	O2-C2-N1	-3.06	119.63	122.79
2	L5	400	A2M	C3'-C2'-C1'	-3.06	96.95	102.81
2	L5	3822	PSU	O2-C2-N1	-3.05	119.64	122.79
2	L5	4590	A2M	O3'-C3'-C2'	3.05	119.72	111.19
2	L5	4523	A2M	C4-N9-C1'	-3.05	119.51	126.63
2	L5	4590	A2M	C4-N9-C1'	-3.05	119.51	126.63
2	L5	1323	A2M	O3'-C3'-C2'	3.04	119.70	111.19
2	L5	4471	PSU	O2-C2-N1	-3.04	119.65	122.79
82	S2	27	A2M	C3'-C2'-C1'	-3.03	97.00	102.81
2	L5	4530	UR3	C6-N1-C2	-3.03	119.32	121.80
2	L5	1677	PSU	O2-C2-N1	-3.03	119.67	122.79
2	L5	3884	PSU	O2-C2-N1	-3.03	119.67	122.79
2	L5	4220	6MZ	N3-C4-N9	3.02	132.31	127.17
2	L5	3920	PSU	O2-C2-N1	-3.02	119.67	122.79
82	S2	627	OMU	O4-C4-C5	-3.02	119.95	125.16
2	L5	3844	PSU	O2-C2-N1	-3.02	119.67	122.79
82	S2	166	A2M	O3'-C3'-C2'	3.02	119.63	111.19
82	S2	1031	A2M	O3'-C3'-C2'	3.01	119.62	111.19
82	S2	651	PSU	O2-C2-N1	-3.01	119.68	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	966	PSU	O2-C2-N1	-3.01	119.68	122.79
82	S2	116	OMU	O4-C4-C5	-3.01	119.97	125.16
82	S2	1232	PSU	O2-C2-N1	-3.01	119.69	122.79
82	S2	1832	6MZ	C5-N7-C8	2.99	108.15	103.45
2	L5	5001	PSU	O2-C2-N1	-2.99	119.70	122.79
82	S2	1639	G7M	C2-N1-C6	-2.98	119.70	125.11
2	L5	3830	A2M	O3'-C3'-C2'	2.98	119.52	111.19
82	S2	1832	6MZ	C4-C5-C6	2.97	119.25	116.78
82	S2	172	OMU	O4-C4-C5	-2.97	120.04	125.16
82	S2	1639	G7M	N9-C4-N3	2.97	131.89	125.95
2	L5	4296	PSU	O2-C2-N1	-2.96	119.74	122.79
2	L5	3825	A2M	O3'-C3'-C2'	2.96	119.46	111.19
82	S2	814	PSU	O2-C2-N1	-2.95	119.74	122.79
2	L5	1871	A2M	C1'-N9-C8	2.94	133.63	127.09
82	S2	799	OMU	C1'-N1-C2	2.94	122.88	117.59
2	L5	4227	OMU	O4-C4-C5	-2.94	120.09	125.16
2	L5	4306	OMU	O4-C4-C5	-2.94	120.09	125.16
4	L8	69	PSU	O2-C2-N1	-2.94	119.76	122.79
82	S2	1832	6MZ	C4-N9-C8	2.93	108.82	105.74
82	S2	801	PSU	C6-N1-C2	-2.93	119.97	122.69
2	L5	2351	OMC	C1'-N1-C6	-2.93	114.53	120.78
82	S2	1367	PSU	O2-C2-N1	-2.92	119.77	122.79
2	L5	400	A2M	C4-N9-C1'	-2.92	119.80	126.63
2	L5	3867	A2M	C2'-C1'-N9	2.91	118.54	113.75
2	L5	1683	PSU	C6-N1-C2	-2.91	119.99	122.69
2	L5	1781	PSU	O2-C2-N1	-2.91	119.79	122.79
82	S2	1031	A2M	C4-N9-C1'	-2.91	119.84	126.63
2	L5	3639	PSU	O2-C2-N1	-2.90	119.79	122.79
82	S2	428	OMU	O4-C4-C5	-2.90	120.17	125.16
82	S2	27	A2M	C4-N9-C1'	-2.89	119.87	126.63
2	L5	3818	UY1	C6-N1-C2	-2.89	120.01	122.69
82	S2	166	A2M	C4-N9-C1'	-2.88	119.89	126.63
82	S2	668	A2M	O3'-C3'-C2'	2.88	119.24	111.19
82	S2	484	A2M	C4-N9-C1'	-2.88	119.90	126.63
2	L5	2815	A2M	C2'-C1'-N9	2.88	118.49	113.75
82	S2	484	A2M	C1'-N9-C8	2.88	133.48	127.09
82	S2	121	OMU	O4-C4-C5	-2.88	120.20	125.16
2	L5	2632	PSU	O2-C2-N1	-2.87	119.82	122.79
2	L5	4521	PSU	O2-C2-N1	-2.87	119.83	122.79
82	S2	1174	PSU	O2-C2-N1	-2.87	119.83	122.79
2	L5	4571	A2M	O3'-C3'-C2'	2.86	119.20	111.19
2	L5	1536	PSU	C6-N1-C2	-2.86	120.03	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3718	A2M	C4-N9-C1'	-2.86	119.95	126.63
82	S2	686	PSU	O2-C2-N1	-2.85	119.84	122.79
2	L5	1524	A2M	C4'-O4'-C1'	-2.85	103.17	109.47
2	L5	4500	PSU	C6-N1-C2	-2.85	120.04	122.69
2	L5	5010	PSU	C6-N1-C2	-2.85	120.04	122.69
2	L5	3695	PSU	O2-C2-N1	-2.85	119.85	122.79
82	S2	863	PSU	O2-C2-N1	-2.85	119.85	122.79
82	S2	1288	OMU	C1'-N1-C2	2.85	122.71	117.59
4	L8	69	PSU	C6-N1-C2	-2.85	120.05	122.69
2	L5	3718	A2M	C1'-N9-C8	2.84	133.41	127.09
2	L5	398	A2M	C4-N9-C1'	-2.84	120.00	126.63
2	L5	4498	OMU	O4-C4-C5	-2.83	120.27	125.16
2	L5	3701	OMC	O2-C2-N3	-2.83	117.86	122.33
2	L5	2401	A2M	C1'-N9-C8	2.83	133.37	127.09
2	L5	4576	PSU	O2-C2-N1	-2.83	119.87	122.79
82	S2	668	A2M	C4-N9-C1'	-2.82	120.03	126.63
82	S2	649	PSU	O2-C2-N1	-2.82	119.88	122.79
82	S2	1244	PSU	O2-C2-N1	-2.82	119.88	122.79
2	L5	1792	PSU	O2-C2-N1	-2.82	119.88	122.79
2	L5	4353	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	2363	A2M	C2'-C1'-N9	2.81	118.38	113.75
2	L5	4532	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	3867	A2M	C4-N9-C1'	-2.81	120.06	126.63
82	S2	105	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	4312	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	4293	PSU	C6-N1-C2	-2.81	120.09	122.69
2	L5	3851	PSU	O2-C2-N1	-2.81	119.89	122.79
2	L5	3884	PSU	C6-N1-C2	-2.81	120.09	122.69
82	S2	1639	G7M	CN7-N7-C8	-2.81	120.54	124.79
2	L5	3844	PSU	C6-N1-C2	-2.80	120.09	122.69
82	S2	105	PSU	C6-N1-C2	-2.80	120.09	122.69
82	S2	1383	A2M	C1'-N9-C8	2.79	133.30	127.09
2	L5	4523	A2M	C1'-N9-C8	2.79	133.29	127.09
2	L5	2815	A2M	O3'-C3'-C2'	2.79	118.99	111.19
2	L5	4431	PSU	O2-C2-N1	-2.78	119.92	122.79
2	L5	4590	A2M	C1'-N9-C8	2.78	133.26	127.09
2	L5	3785	A2M	C4'-O4'-C1'	-2.78	103.33	109.47
82	S2	99	A2M	C4-N9-C1'	-2.78	120.14	126.63
2	L5	1781	PSU	C6-N1-C2	-2.77	120.12	122.69
2	L5	4620	OMU	O4-C4-C5	-2.76	120.40	125.16
82	S2	681	PSU	O2-C2-N1	-2.75	119.95	122.79
82	S2	1004	PSU	C6-N1-C2	-2.75	120.14	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	468	A2M	C1'-N9-C8	2.75	133.20	127.09
2	L5	4442	PSU	O2-C2-N1	-2.75	119.95	122.79
2	L5	4361	PSU	O2-C2-N1	-2.75	119.95	122.79
2	L5	1744	PSU	C6-N1-C2	-2.75	120.14	122.69
2	L5	3808	OMC	C1'-N1-C2	2.74	124.49	118.44
82	S2	1056	PSU	O2-C2-N1	-2.73	119.97	122.79
2	L5	400	A2M	C1'-N9-C8	2.73	133.16	127.09
82	S2	159	A2M	C1'-N9-C8	2.73	133.16	127.09
2	L5	3639	PSU	C6-N1-C2	-2.73	120.16	122.69
2	L5	3785	A2M	O3'-C3'-C2'	2.73	118.83	111.19
82	S2	799	OMU	O4-C4-C5	-2.73	120.46	125.16
2	L5	4973	PSU	O2-C2-N1	-2.73	119.97	122.79
82	S2	159	A2M	C4-N9-C1'	-2.73	120.25	126.63
2	L5	4220	6MZ	C4-C5-C6	2.72	119.04	116.78
2	L5	1871	A2M	O3'-C3'-C2'	2.72	118.80	111.19
2	L5	3825	A2M	C4-N9-C1'	-2.72	120.28	126.63
82	S2	428	OMU	O2-C2-N1	-2.71	119.27	122.80
82	S2	1046	PSU	O2-C2-N1	-2.71	120.00	122.79
2	L5	4220	6MZ	C5-C6-N1	2.71	121.06	118.15
2	L5	400	A2M	O3'-C3'-C2'	2.71	118.76	111.19
2	L5	3822	PSU	C6-C5-C4	2.70	120.00	118.17
82	S2	668	A2M	C1'-N9-C8	2.69	133.07	127.09
2	L5	3867	A2M	C1'-N9-C8	2.69	133.06	127.09
82	S2	1031	A2M	C1'-N9-C8	2.69	133.06	127.09
2	L5	3920	PSU	C6-N1-C2	-2.69	120.20	122.69
2	L5	4571	A2M	C3'-C2'-C1'	-2.69	97.67	102.81
2	L5	1326	A2M	O3'-C3'-C2'	2.68	118.70	111.19
2	L5	4628	PSU	C6-N1-C2	-2.67	120.21	122.69
82	S2	866	PSU	O2-C2-N1	-2.67	120.03	122.79
82	S2	27	A2M	C1'-N9-C8	2.67	133.01	127.09
82	S2	1288	OMU	O4-C4-C5	-2.66	120.57	125.16
2	L5	4523	A2M	O3'-C3'-C2'	2.66	118.63	111.19
82	S2	681	PSU	C6-N1-C2	-2.66	120.22	122.69
2	L5	1862	PSU	O2-C2-N1	-2.66	120.05	122.79
2	L5	3825	A2M	C1'-N9-C8	2.66	132.99	127.09
2	L5	4576	PSU	C6-N1-C2	-2.65	120.23	122.69
2	L5	5001	PSU	C6-N1-C2	-2.65	120.23	122.69
2	L5	4579	PSU	O2-C2-N1	-2.65	120.05	122.79
2	L5	2363	A2M	C3'-C2'-C1'	-2.65	97.74	102.81
82	S2	99	A2M	C1'-N9-C8	2.65	132.97	127.09
82	S2	1046	PSU	C6-N1-C2	-2.63	120.25	122.69
82	S2	1248	B8N	O4-C4-N3	-2.63	115.72	119.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4673	PSU	O2-C2-N1	-2.63	120.08	122.79
2	L5	1582	PSU	C6-N1-C2	-2.63	120.25	122.69
2	L5	4471	PSU	C6-N1-C2	-2.63	120.25	122.69
2	L5	2363	A2M	C1'-N9-C8	2.63	132.92	127.09
82	S2	651	PSU	C6-N1-C2	-2.63	120.25	122.69
2	L5	3785	A2M	C4-N9-C1'	-2.62	120.49	126.63
82	S2	814	PSU	C6-N1-C2	-2.62	120.26	122.69
2	L5	2363	A2M	C4-N9-C1'	-2.61	120.52	126.63
2	L5	2787	A2M	C4-N9-C1'	-2.61	120.53	126.63
2	L5	4442	PSU	C6-N1-C2	-2.61	120.27	122.69
2	L5	4312	PSU	C6-N1-C2	-2.60	120.27	122.69
82	S2	966	PSU	C6-N1-C2	-2.60	120.27	122.69
82	S2	166	A2M	C1'-N9-C8	2.60	132.87	127.09
2	L5	1744	PSU	O2-C2-N1	-2.60	120.11	122.79
2	L5	398	A2M	C1'-N9-C8	2.60	132.86	127.09
2	L5	3867	A2M	C3'-C2'-C1'	-2.59	97.84	102.81
82	S2	1045	PSU	O2-C2-N1	-2.59	120.11	122.79
2	L5	1582	PSU	O2-C2-N1	-2.58	120.13	122.79
2	L5	4457	PSU	C6-N1-C2	-2.58	120.30	122.69
82	S2	1081	PSU	O2-C2-N1	-2.58	120.13	122.79
2	L5	2787	A2M	C1'-N9-C8	2.57	132.81	127.09
2	L5	4431	PSU	C6-N1-C2	-2.57	120.31	122.69
2	L5	3701	OMC	O2-C2-N1	2.56	123.92	118.90
2	L5	4972	PSU	C6-N1-C2	-2.56	120.31	122.69
2	L5	4636	PSU	O2-C2-N1	-2.56	120.15	122.79
82	S2	484	A2M	O3'-C3'-C2'	2.56	118.34	111.19
2	L5	4973	PSU	C6-N1-C2	-2.56	120.32	122.69
2	L5	1860	PSU	O2-C2-N1	-2.55	120.15	122.79
82	S2	1046	PSU	C6-C5-C4	2.55	119.90	118.17
2	L5	1524	A2M	O4'-C1'-C2'	2.55	110.98	106.59
2	L5	3822	PSU	C6-N1-C2	-2.54	120.33	122.69
2	L5	4353	PSU	C6-N1-C2	-2.54	120.33	122.69
82	S2	1367	PSU	C6-N1-C2	-2.54	120.33	122.69
82	S2	109	PSU	C6-N1-C2	-2.54	120.34	122.69
2	L5	4498	OMU	O2-C2-N1	-2.53	119.51	122.80
82	S2	1056	PSU	C6-C5-C4	2.51	119.87	118.17
2	L5	1677	PSU	C6-N1-C2	-2.51	120.36	122.69
2	L5	4457	PSU	O2-C2-N1	-2.51	120.20	122.79
82	S2	93	PSU	O2-C2-N1	-2.50	120.20	122.79
82	S2	1177	PSU	C6-N1-C2	-2.50	120.37	122.69
2	L5	2363	A2M	O3'-C3'-C2'	2.50	118.19	111.19
2	L5	1323	A2M	C3'-C2'-C1'	-2.50	98.01	102.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3822	PSU	O4'-C1'-C2'	2.50	108.61	105.15
2	L5	4361	PSU	C6-N1-C2	-2.50	120.37	122.69
2	L5	2632	PSU	C6-N1-C2	-2.50	120.37	122.69
82	S2	1851	MA6	C1'-N9-C8	-2.50	121.55	127.09
2	L5	4579	PSU	C6-N1-C2	-2.50	120.38	122.69
2	L5	3853	PSU	C6-N1-C2	-2.49	120.38	122.69
82	S2	1232	PSU	C6-N1-C2	-2.48	120.39	122.69
2	L5	1677	PSU	C6-C5-C4	2.48	119.85	118.17
82	S2	1337	4AC	N4-C4-N3	2.47	117.88	113.87
2	L5	3785	A2M	C3'-C2'-C1'	-2.47	98.07	102.81
82	S2	1174	PSU	C6-N1-C2	-2.47	120.40	122.69
2	L5	4500	PSU	C6-C5-C4	2.47	119.84	118.17
2	L5	3825	A2M	C2'-C1'-N9	2.46	117.81	113.75
2	L5	1792	PSU	C6-N1-C2	-2.46	120.41	122.69
2	L5	4456	OMC	C1'-N1-C2	2.46	123.88	118.44
2	L5	2815	A2M	O4'-C1'-C2'	2.46	110.82	106.59
2	L5	3851	PSU	C6-N1-C2	-2.46	120.41	122.69
2	L5	3785	A2M	C2-N1-C6	-2.45	114.71	118.73
2	L5	2839	PSU	O2-C2-N1	-2.45	120.27	122.79
2	L5	3867	A2M	O3'-C3'-C2'	2.44	118.03	111.19
82	S2	93	PSU	C6-N1-C2	-2.44	120.42	122.69
82	S2	649	PSU	C6-N1-C2	-2.44	120.42	122.69
2	L5	1326	A2M	C4-N9-C1'	-2.44	120.92	126.63
4	L8	55	PSU	O2-C2-N1	-2.44	120.27	122.79
82	S2	1177	PSU	O2-C2-N1	-2.44	120.27	122.79
2	L5	3830	A2M	C4-N9-C1'	-2.44	120.93	126.63
82	S2	576	A2M	C4-N9-C1'	-2.43	120.94	126.63
2	L5	4227	OMU	O2-C2-N1	-2.43	119.63	122.80
2	L5	3785	A2M	C1'-N9-C8	2.43	132.49	127.09
2	L5	1323	A2M	C4-N9-C1'	-2.43	120.95	126.63
2	L5	2787	A2M	O4'-C1'-C2'	2.43	110.77	106.59
2	L5	3637	PSU	C6-N1-C2	-2.43	120.44	122.69
82	S2	668	A2M	O4'-C1'-C2'	2.43	110.77	106.59
2	L5	1326	A2M	C1'-N9-C8	2.42	132.46	127.09
82	S2	1639	G7M	N9-C8-N7	-2.41	106.64	112.48
2	L5	3925	OMU	O2-C2-N1	-2.40	119.67	122.80
82	S2	406	PSU	C6-N1-C2	-2.40	120.47	122.69
82	S2	686	PSU	C6-N1-C2	-2.40	120.47	122.69
2	L5	4403	PSU	C6-C5-C4	2.39	119.79	118.17
2	L5	1323	A2M	C1'-N9-C8	2.39	132.40	127.09
2	L5	3830	A2M	C1'-N9-C8	2.38	132.38	127.09
2	L5	4571	A2M	C4-N9-C1'	-2.38	121.06	126.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	1056	PSU	C6-N1-C2	-2.38	120.48	122.69
2	L5	2824	OMC	C1'-N1-C2	2.38	123.70	118.44
82	S2	1832	6MZ	C5-C6-N1	2.37	120.70	118.15
2	L5	4442	PSU	O4'-C1'-C2'	2.37	108.43	105.15
2	L5	4296	PSU	C6-N1-C2	-2.36	120.50	122.69
2	L5	3785	A2M	C5-C6-N1	2.36	123.49	117.51
2	L5	2422	OMC	C1'-N1-C2	2.35	123.64	118.44
82	S2	1248	B8N	O4-C4-C5	-2.35	118.51	122.58
2	L5	4442	PSU	C6-C5-C4	2.35	119.76	118.17
2	L5	2839	PSU	C6-N1-C2	-2.35	120.51	122.69
82	S2	866	PSU	C6-C5-C4	2.35	119.76	118.17
2	L5	2861	OMC	C1'-N1-C2	2.35	123.62	118.44
2	L5	4299	PSU	O2-C2-N1	-2.35	120.37	122.79
2	L5	1524	A2M	C4-N9-C1'	-2.35	121.15	126.63
2	L5	1871	A2M	C6-C5-C4	-2.34	113.98	117.18
82	S2	1383	A2M	C6-C5-C4	-2.33	113.99	117.18
82	S2	866	PSU	C6-N1-C2	-2.33	120.53	122.69
2	L5	1534	A2M	C4-N9-C1'	-2.33	121.17	126.63
2	L5	4532	PSU	C6-N1-C2	-2.33	120.53	122.69
82	S2	1391	OMC	C1'-N1-C2	2.33	123.59	118.44
2	L5	3818	UY1	O2-C2-N1	-2.33	120.38	122.79
2	L5	1323	A2M	O4'-C1'-C2'	2.32	110.58	106.59
2	L5	1534	A2M	C1'-N9-C8	2.32	132.24	127.09
2	L5	2815	A2M	C4-N9-C1'	-2.31	121.22	126.63
82	S2	121	OMU	O2-C2-N1	-2.31	119.78	122.80
2	L5	1326	A2M	C2'-C1'-N9	2.31	117.55	113.75
2	L5	4403	PSU	O4'-C1'-C2'	2.30	108.34	105.15
82	S2	1248	B8N	O4'-C1'-C2'	2.30	108.34	105.15
2	L5	4403	PSU	C6-N1-C2	-2.30	120.56	122.69
82	S2	354	OMU	O2-C2-N1	-2.30	119.81	122.80
82	S2	576	A2M	C1'-N9-C8	2.30	132.19	127.09
2	L5	2787	A2M	O4'-C4'-C3'	2.29	109.71	105.15
82	S2	166	A2M	C6-C5-C4	-2.29	114.05	117.18
82	S2	1326	OMU	O2-C2-N1	-2.29	119.82	122.80
2	L5	1524	A2M	C1'-N9-C8	2.29	132.17	127.09
82	S2	406	PSU	C6-C5-C4	2.28	119.71	118.17
2	L5	3867	A2M	C2-N1-C6	-2.28	114.99	118.73
2	L5	4590	A2M	C6-C5-C4	-2.28	114.07	117.18
2	L5	4521	PSU	C6-N1-C2	-2.27	120.58	122.69
82	S2	1850	MA6	C1'-N9-C8	-2.27	122.06	127.09
82	S2	468	A2M	C6-C5-C4	-2.26	114.09	117.18
82	S2	1081	PSU	C6-N1-C2	-2.26	120.59	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4493	PSU	O2-C2-N1	-2.26	120.45	122.79
2	L5	1326	A2M	C3'-C2'-C1'	-2.26	98.48	102.81
2	L5	4523	A2M	C6-C5-C4	-2.26	114.09	117.18
82	S2	166	A2M	O4'-C1'-C2'	2.24	110.45	106.59
2	L5	1860	PSU	C6-N1-C2	-2.24	120.61	122.69
2	L5	2815	A2M	C1'-N9-C8	2.24	132.06	127.09
2	L5	400	A2M	C6-C5-C4	-2.24	114.12	117.18
2	L5	4620	OMU	O2-C2-N1	-2.24	119.89	122.80
2	L5	4493	PSU	C6-N1-C2	-2.24	120.62	122.69
82	S2	1031	A2M	O4'-C1'-C2'	2.23	110.44	106.59
82	S2	27	A2M	O4'-C1'-C2'	2.23	110.43	106.59
2	L5	2401	A2M	C6-C5-C4	-2.23	114.13	117.18
82	S2	1244	PSU	C6-N1-C2	-2.23	120.62	122.69
2	L5	4571	A2M	C1'-N9-C8	2.23	132.04	127.09
2	L5	1322	1MA	CM1-N1-C6	-2.22	116.71	120.15
2	L5	2363	A2M	C2-N1-C6	-2.21	115.10	118.73
2	L5	3830	A2M	C5-C6-N1	2.21	123.11	117.51
2	L5	3785	A2M	O4'-C4'-C3'	2.20	109.53	105.15
2	L5	4552	PSU	C6-N1-C2	-2.20	120.65	122.69
2	L5	1782	PSU	O2-C2-N1	-2.20	120.52	122.79
82	S2	1383	A2M	C4'-O4'-C1'	-2.19	104.62	109.47
4	L8	55	PSU	C6-N1-C2	-2.19	120.66	122.69
2	L5	4590	A2M	O4'-C1'-C2'	2.19	110.36	106.59
82	S2	1081	PSU	O4'-C1'-C2'	2.19	108.18	105.15
2	L5	398	A2M	C6-C5-C4	-2.18	114.20	117.18
82	S2	1045	PSU	C6-N1-C2	-2.18	120.67	122.69
82	S2	863	PSU	C6-N1-C2	-2.18	120.67	122.69
82	S2	1031	A2M	C6-C5-C4	-2.18	114.20	117.18
2	L5	4571	A2M	O4'-C1'-C2'	2.18	110.34	106.59
2	L5	3830	A2M	C2-N1-C6	-2.18	115.16	118.73
2	L5	1534	A2M	O3'-C3'-C4'	-2.17	104.86	111.08
2	L5	1322	1MA	N1-C6-N6	2.17	125.15	119.71
82	S2	1832	6MZ	C9-N6-C6	-2.16	120.84	122.85
2	L5	1534	A2M	C2-N1-C6	-2.16	115.18	118.73
4	L8	69	PSU	O4'-C1'-C2'	2.16	108.14	105.15
2	L5	2815	A2M	C5-C6-N1	2.16	122.99	117.51
2	L5	2787	A2M	C6-C5-C4	-2.16	114.23	117.18
2	L5	3695	PSU	O4'-C1'-C2'	2.16	108.13	105.15
2	L5	3867	A2M	C6-C5-C4	-2.15	114.24	117.18
2	L5	1326	A2M	O4'-C1'-C2'	2.15	110.30	106.59
82	S2	159	A2M	O4'-C1'-C2'	2.15	110.29	106.59
2	L5	2837	OMU	O2-C2-N1	-2.15	120.00	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	4673	PSU	C6-N1-C2	-2.15	120.69	122.69
82	S2	484	A2M	O4'-C1'-C2'	2.15	110.29	106.59
2	L5	3785	A2M	C6-C5-C4	-2.15	114.24	117.18
2	L5	3718	A2M	C6-C5-C4	-2.15	114.25	117.18
2	L5	3825	A2M	C6-C5-C4	-2.15	114.25	117.18
2	L5	3695	PSU	C6-N1-C2	-2.14	120.70	122.69
2	L5	1326	A2M	C5-C6-N1	2.14	122.95	117.51
2	L5	400	A2M	O4'-C1'-C2'	2.14	110.27	106.59
2	L5	1534	A2M	C5-C6-N1	2.14	122.95	117.51
82	S2	27	A2M	C5-C6-N1	2.14	122.95	117.51
2	L5	1871	A2M	O4'-C1'-C2'	2.14	110.27	106.59
2	L5	1326	A2M	C2-N1-C6	-2.13	115.22	118.73
2	L5	4523	A2M	C4'-O4'-C1'	-2.13	104.75	109.47
2	L5	1323	A2M	C6-C5-C4	-2.13	114.26	117.18
2	L5	4571	A2M	C2-N1-C6	-2.13	115.23	118.73
82	S2	109	PSU	C6-C5-C4	2.13	119.61	118.17
82	S2	468	A2M	O4'-C1'-C2'	2.13	110.25	106.59
82	S2	166	A2M	C5-C6-N1	2.13	122.92	117.51
82	S2	159	A2M	O3'-C3'-C4'	-2.13	104.98	111.08
2	L5	4636	PSU	O4'-C1'-C2'	2.12	108.09	105.15
2	L5	2363	A2M	C5-C6-N1	2.12	122.90	117.51
82	S2	27	A2M	C6-C5-C4	-2.12	114.28	117.18
2	L5	4457	PSU	O4'-C1'-C2'	2.12	108.08	105.15
2	L5	400	A2M	C2'-C1'-N9	2.12	117.23	113.75
4	L8	69	PSU	C6-C5-C4	2.11	119.60	118.17
82	S2	668	A2M	C6-C5-C4	-2.11	114.30	117.18
2	L5	4689	PSU	C6-C5-C4	2.11	119.59	118.17
82	S2	116	OMU	O2-C2-N1	-2.10	120.06	122.80
2	L5	400	A2M	C5-C6-N1	2.10	122.85	117.51
82	S2	1031	A2M	C5-C6-N1	2.10	122.85	117.51
2	L5	2815	A2M	C3'-C2'-C1'	-2.10	98.79	102.81
82	S2	159	A2M	C3'-C2'-C1'	-2.09	98.80	102.81
2	L5	3830	A2M	C6-C5-C4	-2.09	114.32	117.18
82	S2	99	A2M	C6-C5-C4	-2.09	114.32	117.18
2	L5	1862	PSU	C6-N1-C2	-2.09	120.75	122.69
82	S2	159	A2M	C2-N1-C6	-2.09	115.30	118.73
82	S2	668	A2M	C2-N1-C6	-2.09	115.30	118.73
82	S2	1046	PSU	O4'-C1'-C2'	2.09	108.04	105.15
2	L5	2815	A2M	C2-N1-C6	-2.09	115.30	118.73
2	L5	2787	A2M	C5-C6-N1	2.08	122.81	117.51
2	L5	3782	5MC	C1'-N1-C6	-2.08	117.72	121.15
2	L5	4636	PSU	C6-C5-C4	2.08	119.58	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L5	3825	A2M	C2-N1-C6	-2.08	115.31	118.73
2	L5	1323	A2M	C5-C6-N1	2.08	122.80	117.51
2	L5	3867	A2M	C5-C6-N1	2.08	122.79	117.51
82	S2	484	A2M	C5-C6-N1	2.08	122.79	117.51
82	S2	159	A2M	C5-C6-N1	2.08	122.79	117.51
82	S2	651	PSU	C6-C5-C4	2.07	119.57	118.17
2	L5	398	A2M	C5-C6-N1	2.07	122.78	117.51
2	L5	4552	PSU	C6-C5-C4	2.07	119.57	118.17
82	S2	27	A2M	C2-N1-C6	-2.07	115.33	118.73
2	L5	4973	PSU	C6-C5-C4	2.07	119.57	118.17
2	L5	1326	A2M	C6-C5-C4	-2.07	114.35	117.18
2	L5	1323	A2M	C2-N1-C6	-2.07	115.33	118.73
2	L5	3808	OMC	C1'-N1-C6	-2.07	116.36	120.78
82	S2	627	OMU	O2-C2-N1	-2.07	120.11	122.80
82	S2	1383	A2M	C5-C6-N1	2.07	122.76	117.51
82	S2	484	A2M	C6-C5-C4	-2.07	114.36	117.18
82	S2	1248	B8N	C31-N3-C4	2.07	120.10	117.18
2	L5	1524	A2M	C6-C5-C4	-2.07	114.36	117.18
2	L5	2401	A2M	C5-C6-N1	2.06	122.75	117.51
82	S2	99	A2M	C2-N1-C6	-2.06	115.34	118.73
82	S2	1031	A2M	C2-N1-C6	-2.06	115.35	118.73
2	L5	3825	A2M	C5-C6-N1	2.06	122.73	117.51
2	L5	4571	A2M	C5-C6-N1	2.06	122.73	117.51
2	L5	1871	A2M	C5-C6-N1	2.06	122.73	117.51
82	S2	99	A2M	C5-C6-N1	2.06	122.73	117.51
82	S2	468	A2M	C5-C6-N1	2.05	122.73	117.51
2	L5	4972	PSU	C6-C5-C4	2.05	119.56	118.17
2	L5	1744	PSU	C6-C5-C4	2.05	119.56	118.17
2	L5	398	A2M	O4'-C1'-C2'	2.05	110.12	106.59
2	L5	4590	A2M	C5-C6-N1	2.04	122.70	117.51
82	S2	159	A2M	C6-C5-C4	-2.04	114.39	117.18
2	L5	1744	PSU	O4'-C1'-C2'	2.04	107.98	105.15
2	L5	398	A2M	C2-N1-C6	-2.04	115.38	118.73
2	L5	400	A2M	C2-N1-C6	-2.04	115.38	118.73
2	L5	4523	A2M	C5-C6-N1	2.04	122.68	117.51
2	L5	4636	PSU	C6-N1-C2	-2.03	120.81	122.69
2	L5	2787	A2M	C2-N1-C6	-2.03	115.40	118.73
2	L5	1524	A2M	C2-N1-C6	-2.02	115.41	118.73
82	S2	484	A2M	C2-N1-C6	-2.02	115.41	118.73
82	S2	576	A2M	C6-C5-C4	-2.02	114.42	117.18
2	L5	1782	PSU	C6-N1-C2	-2.02	120.82	122.69
2	L5	3830	A2M	C4'-O4'-C1'	-2.02	105.01	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	S2	576	A2M	C5-C6-N1	2.01	122.63	117.51
2	L5	1534	A2M	CM'-O2'-C2'	-2.01	109.30	114.47
2	L5	4220	6MZ	C4-C5-N7	-2.01	108.28	110.58
2	L5	1524	A2M	C5-C6-N1	2.01	122.62	117.51
2	L5	4306	OMU	O2-C2-N1	-2.01	120.18	122.80
2	L5	3920	PSU	C6-C5-C4	2.01	119.53	118.17
2	L5	4299	PSU	C6-N1-C2	-2.01	120.83	122.69
2	L5	1871	A2M	C4'-O4'-C1'	-2.00	105.04	109.47
2	L5	1524	A2M	CM'-O2'-C2'	-2.00	109.33	114.47
2	L5	2401	A2M	C2-N1-C6	-2.00	115.44	118.73
2	L5	4571	A2M	C6-C5-C4	-2.00	114.45	117.18

There are no chirality outliers.

All (154) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L5	400	A2M	C1'-C2'-O2'-CM'
2	L5	1316	OMG	C1'-C2'-O2'-CM2
2	L5	1326	A2M	O4'-C4'-C5'-O5'
2	L5	1340	OMC	C1'-C2'-O2'-CM2
2	L5	1625	OMG	O4'-C4'-C5'-O5'
2	L5	1677	PSU	C2'-C1'-C5-C4
2	L5	2364	OMG	O4'-C4'-C5'-O5'
2	L5	2787	A2M	C1'-C2'-O2'-CM'
2	L5	2861	OMC	C1'-C2'-O2'-CM2
2	L5	3792	OMG	O4'-C4'-C5'-O5'
2	L5	3818	UY1	C1'-C2'-O2'-CM2
2	L5	3867	A2M	C1'-C2'-O2'-CM'
2	L5	3925	OMU	C1'-C2'-O2'-CM2
2	L5	4196	OMG	C1'-C2'-O2'-CM2
2	L5	4220	6MZ	O4'-C4'-C5'-O5'
2	L5	4227	OMU	C1'-C2'-O2'-CM2
2	L5	4620	OMU	C1'-C2'-O2'-CM2
2	L5	4637	OMG	O4'-C4'-C5'-O5'
2	L5	4637	OMG	C1'-C2'-O2'-CM2
82	S2	27	A2M	C1'-C2'-O2'-CM'
82	S2	116	OMU	C1'-C2'-O2'-CM2
82	S2	576	A2M	O4'-C4'-C5'-O5'
82	S2	644	OMG	O4'-C4'-C5'-O5'
82	S2	644	OMG	C1'-C2'-O2'-CM2
82	S2	1248	B8N	C31-C32-C33-C34
82	S2	1272	OMC	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
82	S2	1288	OMU	C1'-C2'-O2'-CM2
82	S2	1288	OMU	O4'-C4'-C5'-O5'
82	S2	1328	OMG	C1'-C2'-O2'-CM2
82	S2	1337	4AC	N3-C4-N4-C7
82	S2	1490	OMG	C1'-C2'-O2'-CM2
82	S2	1832	6MZ	C5-C6-N6-C9
82	S2	1832	6MZ	N1-C6-N6-C9
2	L5	3701	OMC	C2'-C1'-N1-C2
2	L5	1323	A2M	O4'-C4'-C5'-O5'
2	L5	1524	A2M	C3'-C4'-C5'-O5'
2	L5	1781	PSU	C3'-C4'-C5'-O5'
2	L5	2401	A2M	C3'-C4'-C5'-O5'
2	L5	3701	OMC	O4'-C4'-C5'-O5'
2	L5	3899	OMG	O4'-C4'-C5'-O5'
2	L5	3899	OMG	C3'-C4'-C5'-O5'
2	L5	4500	PSU	C3'-C4'-C5'-O5'
2	L5	4500	PSU	O4'-C4'-C5'-O5'
2	L5	4590	A2M	O4'-C4'-C5'-O5'
2	L5	4590	A2M	C3'-C4'-C5'-O5'
82	S2	576	A2M	C3'-C4'-C5'-O5'
82	S2	867	OMG	C3'-C4'-C5'-O5'
82	S2	1272	OMC	C3'-C4'-C5'-O5'
82	S2	1288	OMU	C3'-C4'-C5'-O5'
82	S2	1442	OMU	C3'-C4'-C5'-O5'
82	S2	1442	OMU	O4'-C4'-C5'-O5'
2	L5	398	A2M	O4'-C4'-C5'-O5'
2	L5	1326	A2M	C3'-C4'-C5'-O5'
2	L5	1625	OMG	C3'-C4'-C5'-O5'
2	L5	2401	A2M	O4'-C4'-C5'-O5'
2	L5	2787	A2M	C3'-C4'-C5'-O5'
2	L5	3701	OMC	C3'-C4'-C5'-O5'
2	L5	3792	OMG	C3'-C4'-C5'-O5'
2	L5	3867	A2M	C3'-C4'-C5'-O5'
82	S2	428	OMU	C3'-C4'-C5'-O5'
82	S2	517	OMC	C3'-C4'-C5'-O5'
82	S2	517	OMC	O4'-C4'-C5'-O5'
82	S2	799	OMU	C3'-C4'-C5'-O5'
82	S2	799	OMU	O4'-C4'-C5'-O5'
82	S2	801	PSU	C3'-C4'-C5'-O5'
2	L5	3701	OMC	C2'-C1'-N1-C6
2	L5	4447	5MC	C2'-C1'-N1-C6
82	S2	428	OMU	C2'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
2	L5	4637	OMG	C3'-C4'-C5'-O5'
82	S2	428	OMU	O4'-C4'-C5'-O5'
82	S2	644	OMG	C3'-C4'-C5'-O5'
2	L5	1323	A2M	C3'-C4'-C5'-O5'
2	L5	1524	A2M	O4'-C4'-C5'-O5'
2	L5	1536	PSU	C3'-C4'-C5'-O5'
2	L5	2364	OMG	C3'-C4'-C5'-O5'
2	L5	4447	5MC	C2'-C1'-N1-C2
82	S2	428	OMU	C2'-C1'-N1-C2
2	L5	1677	PSU	O4'-C4'-C5'-O5'
2	L5	4220	6MZ	C3'-C4'-C5'-O5'
82	S2	99	A2M	O4'-C4'-C5'-O5'
82	S2	683	OMG	C3'-C4'-C5'-O5'
82	S2	867	OMG	O4'-C4'-C5'-O5'
82	S2	1832	6MZ	O4'-C4'-C5'-O5'
2	L5	2787	A2M	C2'-C1'-N9-C8
2	L5	1677	PSU	C3'-C4'-C5'-O5'
2	L5	1781	PSU	O4'-C4'-C5'-O5'
2	L5	2422	OMC	O4'-C4'-C5'-O5'
82	S2	668	A2M	O4'-C4'-C5'-O5'
82	S2	801	PSU	O4'-C4'-C5'-O5'
2	L5	2422	OMC	C3'-C4'-C5'-O5'
2	L5	3818	UY1	C4'-C5'-O5'-P
2	L5	398	A2M	C3'-C4'-C5'-O5'
2	L5	1536	PSU	O4'-C4'-C5'-O5'
2	L5	3867	A2M	O4'-C4'-C5'-O5'
82	S2	668	A2M	C3'-C4'-C5'-O5'
2	L5	4590	A2M	C4'-C5'-O5'-P
82	S2	1703	OMC	O4'-C4'-C5'-O5'
82	S2	1248	B8N	N34-C33-C34-O36
2	L5	4306	OMU	C1'-C2'-O2'-CM2
82	S2	159	A2M	C1'-C2'-O2'-CM'
2	L5	2787	A2M	O4'-C4'-C5'-O5'
82	S2	1045	PSU	O4'-C4'-C5'-O5'
82	S2	1832	6MZ	C5'-O5'-P-OP2
2	L5	2787	A2M	C2'-C1'-N9-C4
2	L5	2876	OMG	C3'-C4'-C5'-O5'
82	S2	1045	PSU	C3'-C4'-C5'-O5'
82	S2	1248	B8N	C31-C32-C33-N34
2	L5	4447	5MC	O4'-C1'-N1-C2
2	L5	4623	OMG	C3'-C4'-C5'-O5'
82	S2	428	OMU	O4'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
2	L5	4447	5MC	O4'-C1'-N1-C6
2	L5	3701	OMC	O4'-C1'-N1-C6
82	S2	428	OMU	O4'-C1'-N1-C6
2	L5	4494	OMG	C3'-C2'-O2'-CM2
2	L5	4500	PSU	C4'-C5'-O5'-P
82	S2	576	A2M	C4'-C5'-O5'-P
2	L5	1677	PSU	O4'-C1'-C5-C4
2	L5	3818	UY1	O4'-C1'-C5-C4
2	L5	4500	PSU	O4'-C1'-C5-C4
82	S2	1248	B8N	O4'-C1'-C5-C4
82	S2	1639	G7M	C3'-C4'-C5'-O5'
2	L5	1534	A2M	C4'-C5'-O5'-P
2	L5	4623	OMG	O4'-C4'-C5'-O5'
82	S2	1851	MA6	C4'-C5'-O5'-P
82	S2	1490	OMG	C4'-C5'-O5'-P
2	L5	2815	A2M	O4'-C4'-C5'-O5'
82	S2	99	A2M	C3'-C4'-C5'-O5'
2	L5	3701	OMC	O4'-C1'-N1-C2
2	L5	3844	PSU	C4'-C5'-O5'-P
2	L5	3887	OMC	C4'-C5'-O5'-P
82	S2	644	OMG	C4'-C5'-O5'-P
2	L5	2351	OMC	C2'-C1'-N1-C6
2	L5	1322	1MA	C2'-C1'-N9-C8
2	L5	398	A2M	C1'-C2'-O2'-CM'
2	L5	2365	OMC	C1'-C2'-O2'-CM2
2	L5	4590	A2M	C1'-C2'-O2'-CM'
82	S2	468	A2M	C1'-C2'-O2'-CM'
82	S2	576	A2M	C1'-C2'-O2'-CM'
82	S2	601	OMG	C1'-C2'-O2'-CM2
2	L5	1322	1MA	C2'-C1'-N9-C4
2	L5	2632	PSU	C3'-C4'-C5'-O5'
2	L5	4636	PSU	O4'-C1'-C5-C6
82	S2	1248	B8N	O4'-C1'-C5-C6
2	L5	4228	OMG	C3'-C2'-O2'-CM2
2	L5	2876	OMG	O4'-C4'-C5'-O5'
82	S2	1639	G7M	O4'-C4'-C5'-O5'
2	L5	4370	OMG	C3'-C2'-O2'-CM2
2	L5	2632	PSU	O4'-C4'-C5'-O5'
82	S2	683	OMG	O4'-C4'-C5'-O5'
82	S2	1832	6MZ	C3'-C4'-C5'-O5'
2	L5	4636	PSU	C4'-C5'-O5'-P
82	S2	1081	PSU	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
2	L5	2351	OMC	O4'-C4'-C5'-O5'
2	L5	3785	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

89 monomers are involved in 130 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	S2	668	A2M	1	0
82	S2	99	A2M	1	0
2	L5	1323	A2M	1	0
82	S2	1383	A2M	1	0
2	L5	398	A2M	2	0
2	L5	4571	A2M	2	0
2	L5	4618	OMG	1	0
2	L5	1677	PSU	1	0
82	S2	27	A2M	2	0
82	S2	1337	4AC	4	0
82	S2	166	A2M	1	0
82	S2	1850	MA6	2	0
82	S2	627	OMU	1	0
82	S2	116	OMU	1	0
82	S2	1232	PSU	2	0
2	L5	4620	OMU	3	0
2	L5	2365	OMC	1	0
82	S2	1288	OMU	1	0
82	S2	1328	OMG	1	0
2	L5	1316	OMG	1	0
2	L5	4590	A2M	1	0
2	L5	1340	OMC	2	0
2	L5	4493	PSU	1	0
2	L5	4530	UR3	1	0
82	S2	1272	OMC	1	0
82	S2	644	OMG	1	0
2	L5	4532	PSU	1	0
82	S2	109	PSU	1	0
82	S2	121	OMU	1	0
2	L5	4494	OMG	1	0
82	S2	1703	OMC	1	0
2	L5	3841	OMC	1	0
2	L5	3830	A2M	1	0
2	L5	3825	A2M	1	0
2	L5	4353	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	S2	601	OMG	2	0
2	L5	3701	OMC	1	0
2	L5	4471	PSU	1	0
2	L5	3822	PSU	1	0
2	L5	3867	A2M	4	0
2	L5	3785	A2M	2	0
2	L5	4227	OMU	1	0
82	S2	576	A2M	3	0
2	L5	4579	PSU	1	0
2	L5	2351	OMC	2	0
82	S2	1031	A2M	1	0
82	S2	509	OMG	5	0
82	S2	1832	6MZ	1	0
2	L5	4392	OMG	2	0
82	S2	484	A2M	2	0
82	S2	683	OMG	1	0
2	L5	5010	PSU	2	0
2	L5	3869	OMC	1	0
2	L5	3744	OMG	1	0
2	L5	4306	OMU	1	0
2	L5	3884	PSU	1	0
82	S2	1177	PSU	3	0
2	L5	2363	A2M	1	0
2	L5	4637	OMG	1	0
2	L5	2424	OMG	1	0
82	S2	159	A2M	3	0
2	L5	2401	A2M	1	0
2	L5	2632	PSU	1	0
2	L5	3925	OMU	2	0
2	L5	4456	OMC	1	0
82	S2	354	OMU	1	0
82	S2	649	PSU	2	0
2	L5	5001	PSU	1	0
2	L5	4431	PSU	1	0
2	L5	1871	A2M	1	0
2	L5	3792	OMG	1	0
2	L5	4523	A2M	2	0
2	L5	4536	OMC	1	0
2	L5	4196	OMG	1	0
2	L5	3718	A2M	4	0
2	L5	4457	PSU	1	0
82	S2	462	OMC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	S2	1174	PSU	2	0
82	S2	436	OMG	1	0
82	S2	651	PSU	1	0
82	S2	468	A2M	3	0
2	L5	1326	A2M	3	0
2	L5	4636	PSU	1	0
2	L5	4689	PSU	1	0
2	L5	2422	OMC	1	0
2	L5	4447	5MC	1	0
82	S2	1490	OMG	1	0
4	L8	75	OMG	2	0
82	S2	1639	G7M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 242 ligands modelled in this entry, 225 are monoatomic - leaving 17 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
87	SPD	L5	5287	-	9,9,9	0.33	0	8,8,8	0.82	0
86	SPM	L5	5259	-	13,13,13	0.35	0	12,12,12	0.95	0
87	SPD	L5	5283	-	9,9,9	0.32	0	8,8,8	0.84	0
87	SPD	L5	5286	-	9,9,9	0.34	0	8,8,8	0.81	0
87	SPD	L5	5290	-	9,9,9	0.33	0	8,8,8	0.85	0
87	SPD	L5	5284	-	9,9,9	0.33	0	8,8,8	0.80	0
86	SPM	L5	5289	-	13,13,13	0.36	0	12,12,12	0.86	0
87	SPD	L5	5285	-	9,9,9	0.31	0	8,8,8	0.83	0
87	SPD	L5	5261	-	9,9,9	0.31	0	8,8,8	1.00	0
87	SPD	L5	5288	-	9,9,9	0.34	0	8,8,8	0.81	0
87	SPD	L5	5291	-	9,9,9	0.32	0	8,8,8	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	SPD	L5	5293	-	9,9,9	0.35	0	8,8,8	0.80	0
86	SPM	L5	5264	-	13,13,13	0.37	0	12,12,12	1.01	0
86	SPM	L5	5292	-	13,13,13	0.36	0	12,12,12	0.95	0
86	SPM	L5	5294	-	13,13,13	0.36	0	12,12,12	0.73	0
86	SPM	L5	5267	-	13,13,13	0.36	0	12,12,12	0.97	0
86	SPM	L5	5263	-	13,13,13	0.35	0	12,12,12	0.95	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	SPD	L5	5287	-	-	4/7/7/7	-
86	SPM	L5	5259	-	-	2/11/11/11	-
87	SPD	L5	5283	-	-	1/7/7/7	-
87	SPD	L5	5286	-	-	1/7/7/7	-
87	SPD	L5	5290	-	-	3/7/7/7	-
87	SPD	L5	5284	-	-	1/7/7/7	-
86	SPM	L5	5289	-	-	5/11/11/11	-
87	SPD	L5	5285	-	-	3/7/7/7	-
87	SPD	L5	5261	-	-	2/7/7/7	-
87	SPD	L5	5288	-	-	2/7/7/7	-
87	SPD	L5	5291	-	-	3/7/7/7	-
87	SPD	L5	5293	-	-	5/7/7/7	-
86	SPM	L5	5264	-	-	3/11/11/11	-
86	SPM	L5	5292	-	-	5/11/11/11	-
86	SPM	L5	5294	-	-	2/11/11/11	-
86	SPM	L5	5267	-	-	3/11/11/11	-
86	SPM	L5	5263	-	-	2/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
87	L5	5293	SPD	C3-C4-C5-N6

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Mol	Chain	Res	Type	Atoms
86	L5	5292	SPM	C7-C8-C9-N10
86	L5	5294	SPM	N10-C11-C12-C13
87	L5	5290	SPD	N6-C7-C8-C9
86	L5	5264	SPM	N5-C6-C7-C8
87	L5	5293	SPD	N6-C7-C8-C9
86	L5	5289	SPM	C7-C8-C9-N10
87	L5	5285	SPD	C3-C4-C5-N6
86	L5	5289	SPM	C12-C11-N10-C9
86	L5	5292	SPM	N10-C11-C12-C13
86	L5	5264	SPM	C7-C6-N5-C4
86	L5	5259	SPM	N5-C6-C7-C8
86	L5	5267	SPM	C6-C7-C8-C9
86	L5	5289	SPM	C6-C7-C8-C9
87	L5	5285	SPD	N6-C7-C8-C9
87	L5	5288	SPD	C2-C3-C4-C5
86	L5	5263	SPM	C6-C7-C8-C9
87	L5	5285	SPD	C2-C3-C4-C5
86	L5	5259	SPM	C6-C7-C8-C9
87	L5	5293	SPD	C2-C3-C4-C5
87	L5	5291	SPD	N6-C7-C8-C9
87	L5	5286	SPD	C3-C4-C5-N6
86	L5	5292	SPM	N5-C6-C7-C8
87	L5	5284	SPD	C3-C4-C5-N6
87	L5	5288	SPD	C8-C7-N6-C5
87	L5	5261	SPD	C2-C3-C4-C5
86	L5	5289	SPM	N1-C2-C3-C4
87	L5	5291	SPD	C4-C5-N6-C7
87	L5	5290	SPD	N1-C2-C3-C4
86	L5	5267	SPM	C2-C3-C4-N5
87	L5	5261	SPD	N6-C7-C8-C9
86	L5	5267	SPM	C8-C9-N10-C11
87	L5	5290	SPD	C2-C3-C4-C5
87	L5	5283	SPD	C2-C3-C4-C5
87	L5	5287	SPD	C4-C5-N6-C7
87	L5	5293	SPD	C8-C7-N6-C5
86	L5	5264	SPM	N10-C11-C12-C13
87	L5	5287	SPD	C8-C7-N6-C5
87	L5	5287	SPD	C3-C4-C5-N6
86	L5	5289	SPM	C7-C6-N5-C4
86	L5	5292	SPM	C8-C9-N10-C11
86	L5	5294	SPM	C8-C9-N10-C11
87	L5	5293	SPD	C4-C5-N6-C7

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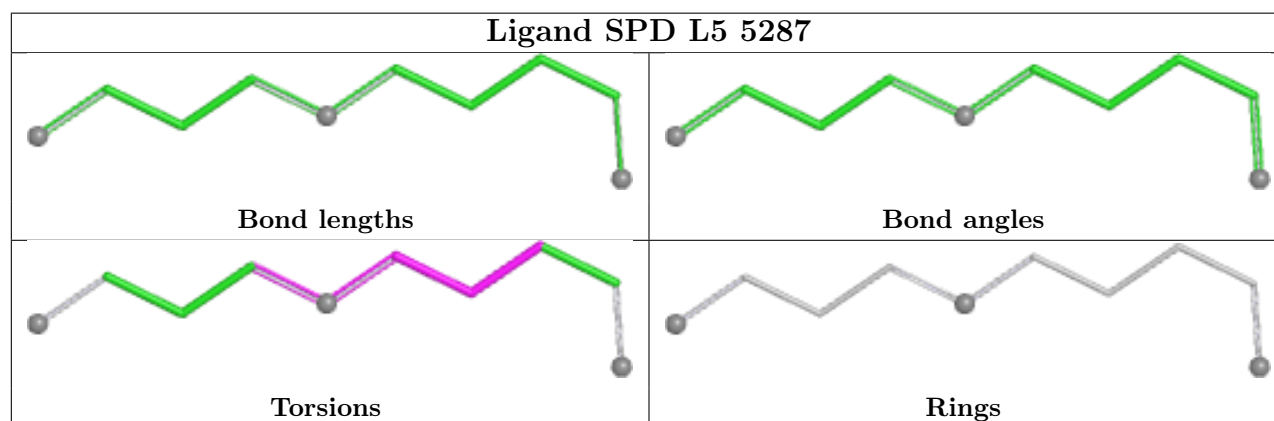
Mol	Chain	Res	Type	Atoms
86	L5	5292	SPM	C7-C6-N5-C4
87	L5	5291	SPD	C8-C7-N6-C5
87	L5	5287	SPD	C2-C3-C4-C5
86	L5	5263	SPM	C8-C9-N10-C11

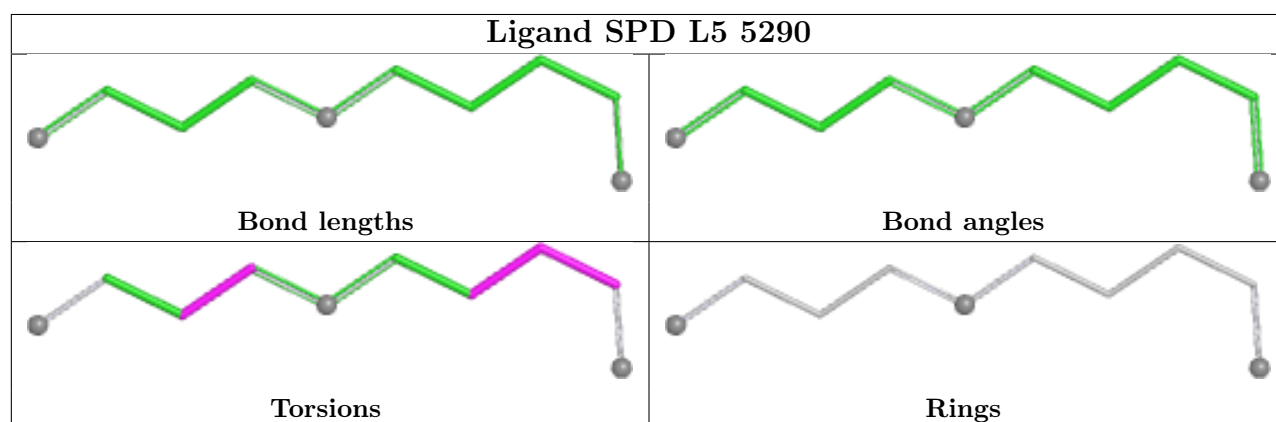
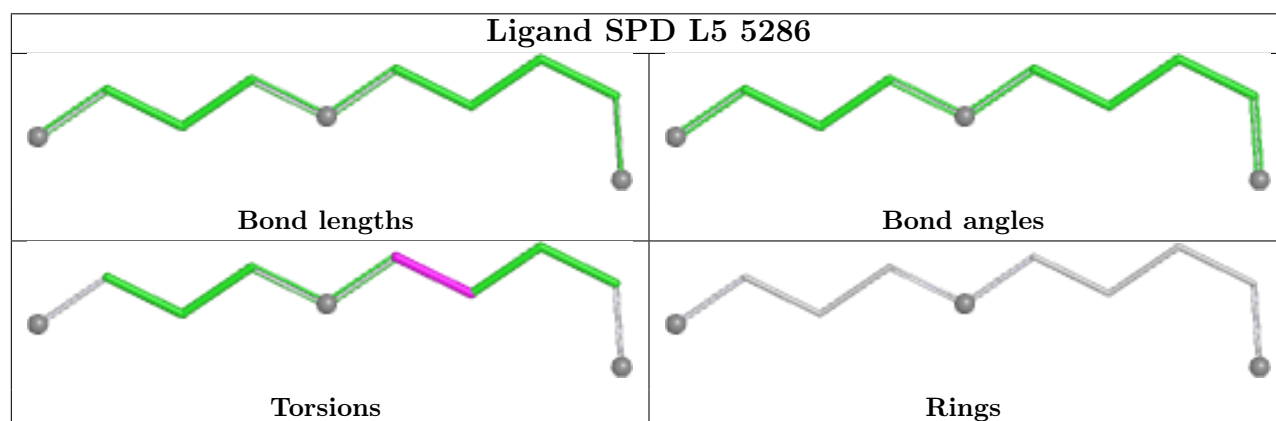
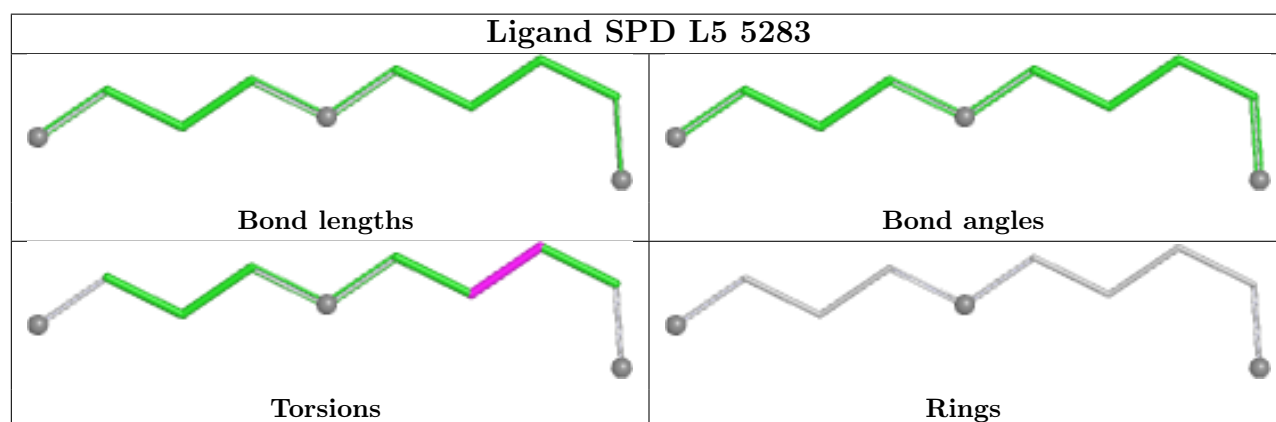
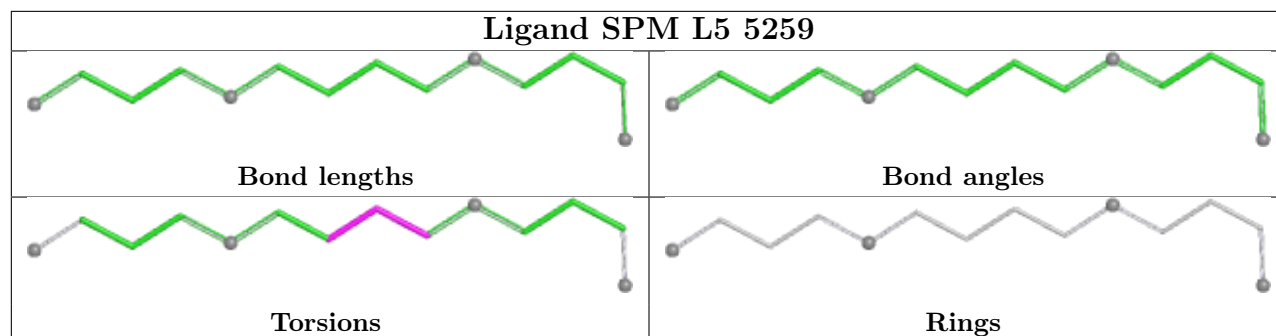
There are no ring outliers.

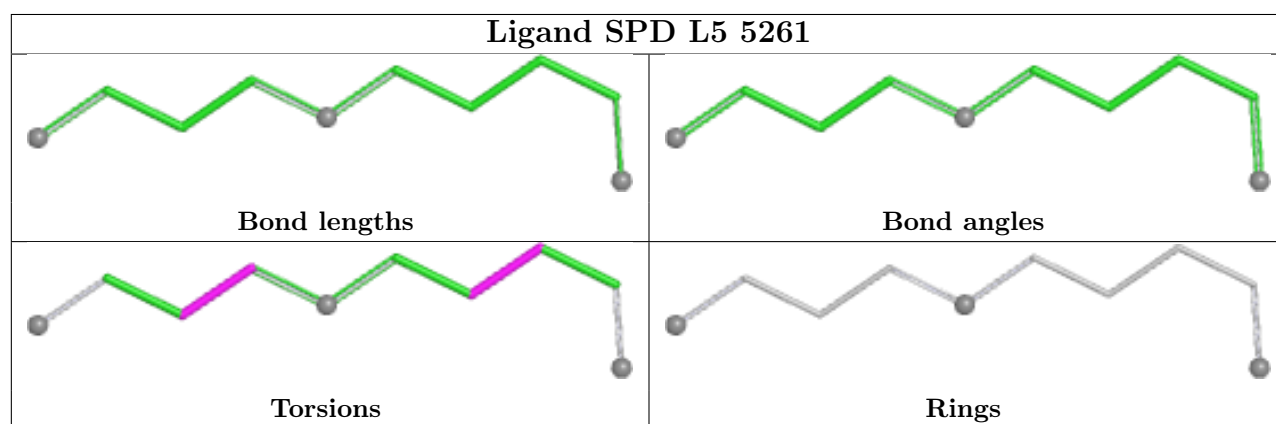
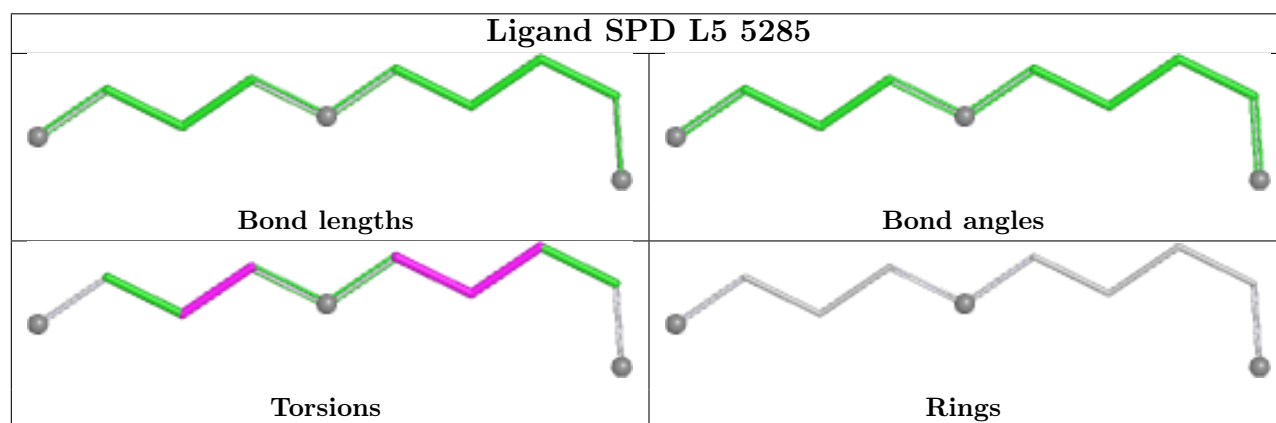
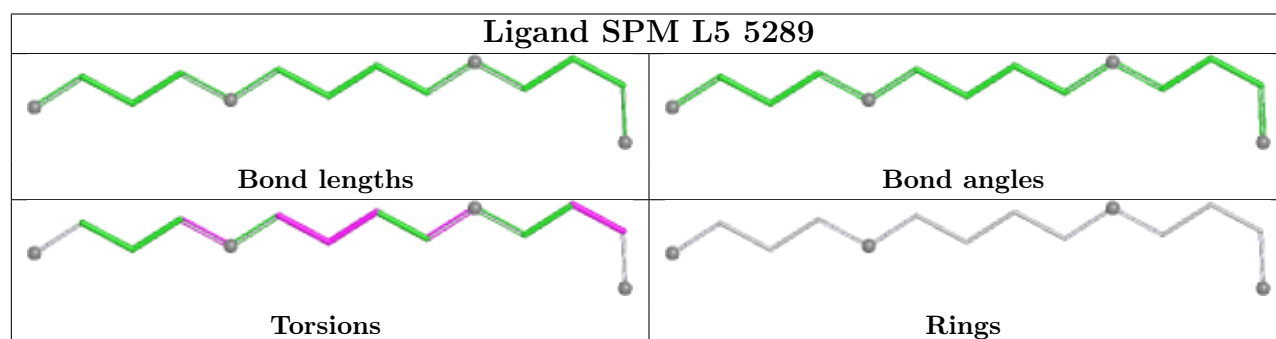
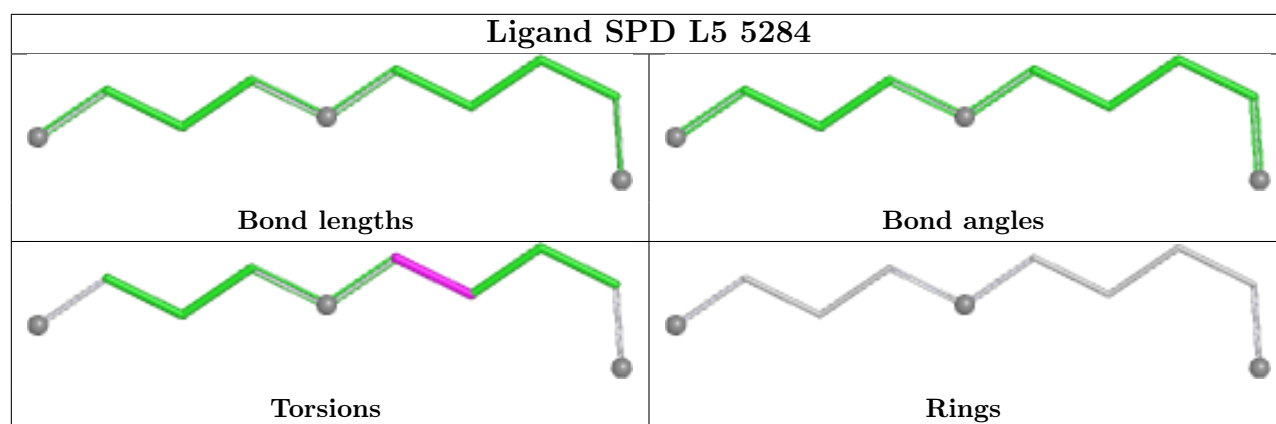
8 monomers are involved in 11 short contacts:

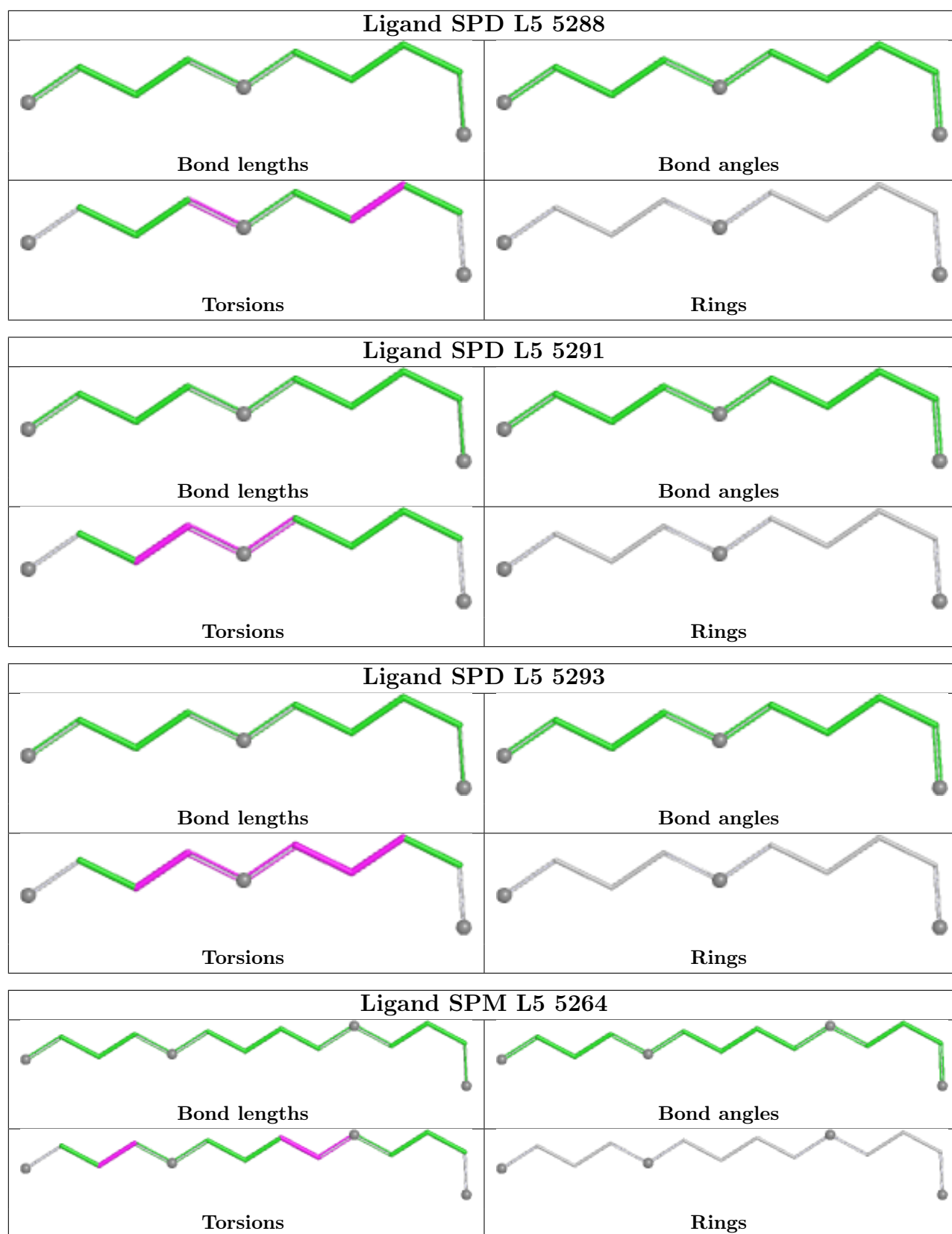
Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	L5	5287	SPD	1	0
87	L5	5286	SPD	1	0
86	L5	5289	SPM	1	0
87	L5	5293	SPD	1	0
86	L5	5264	SPM	2	0
86	L5	5292	SPM	1	0
86	L5	5294	SPM	2	0
86	L5	5263	SPM	2	0

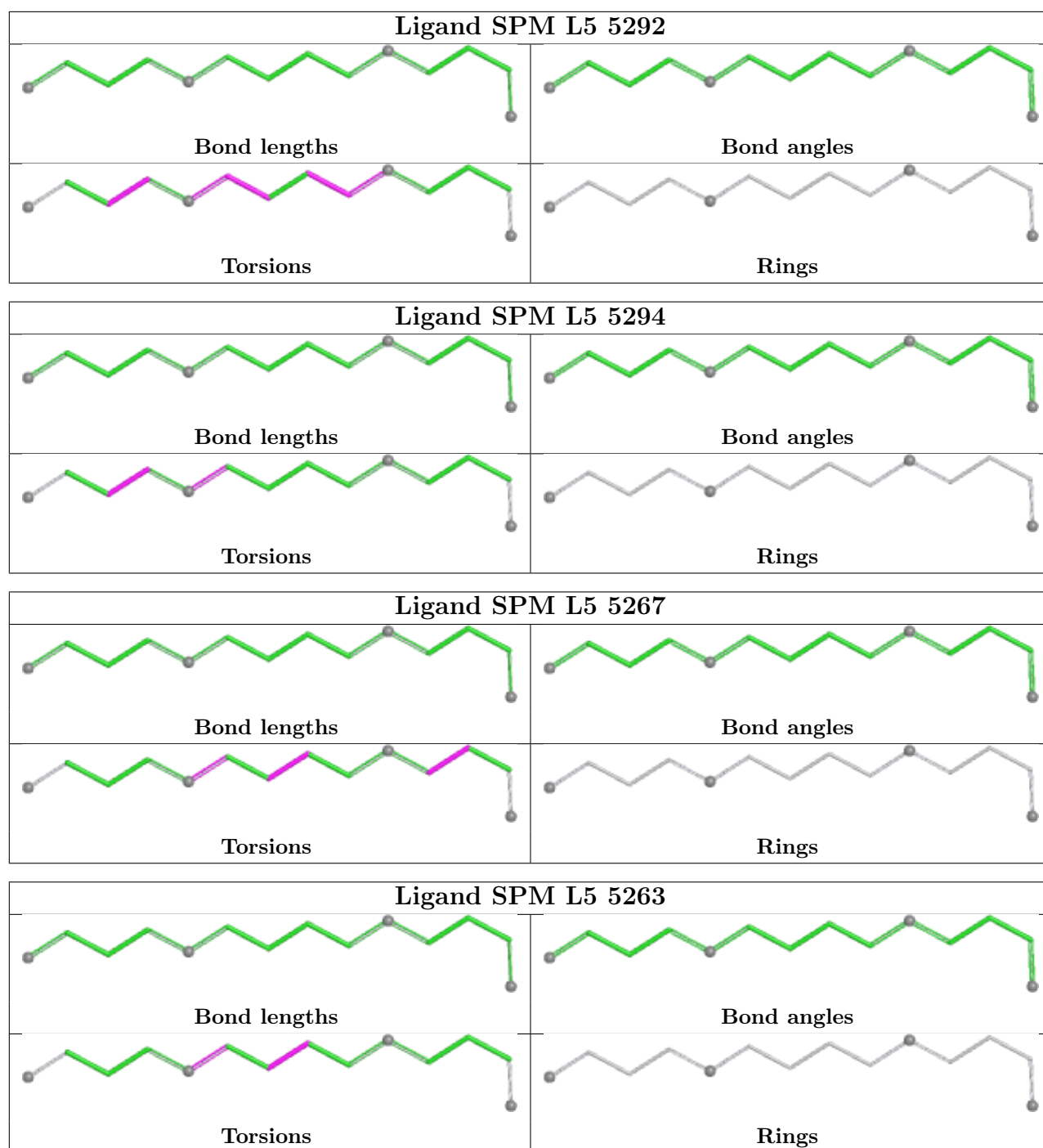
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	L5	10
82	S2	5
31	Lb	1
9	LE	1
48	Lt	1
69	SH	1
1	Pt	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:VAL	N	34.07
1	S2	753:C	O3'	785:C	P	28.56
1	LE	76:ALA	C	87:LYS	N	23.14
1	L5	1706:A	O3'	1716:G	P	21.24
1	L5	2910:G	O3'	3584:C	P	20.98
1	L5	760:G	O3'	903:C	P	17.02
1	L5	519:C	O3'	642:G	P	15.66
1	S2	698:G	O3'	730:C	P	15.60
1	Lt	87:GLU	C	104:ILE	N	15.01
1	L5	4776:G	O3'	4858:C	P	14.77
1	L5	2112:G	O3'	2249:C	P	14.24
1	L5	3954:A	O3'	4056:A	P	13.37
1	S2	739:C	O3'	746:C	P	12.95
1	L5	990:C	O3'	1064:G	P	12.13
1	SH	107:LYS	C	111:LYS	N	11.37
1	Pt	15:G	O3'	18:G	P	9.79
1	L5	1222:A	O3'	1234:G	P	9.47
1	S2	225:G	O3'	287:U	P	8.09
1	L5	1100:U	O3'	1167:C	P	6.70
1	S2	1831:A	O3'	1832:6MZ	P	4.24

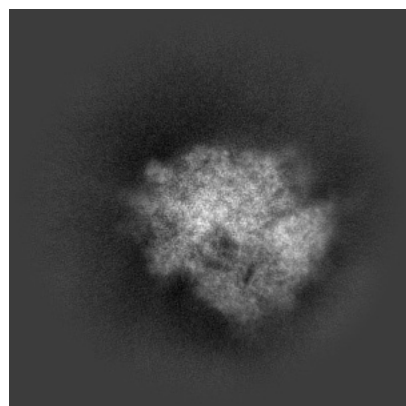
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71329. These allow visual inspection of the internal detail of the map and identification of artifacts.

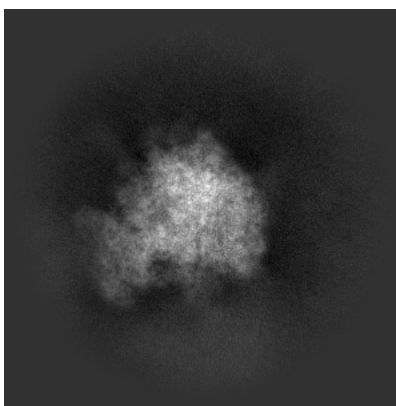
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

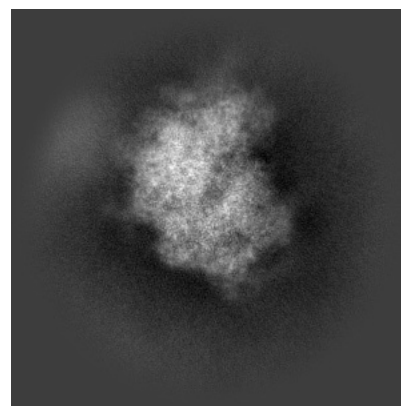
6.1.1 Primary map



X

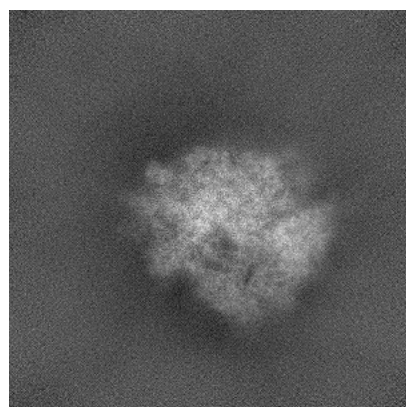


Y

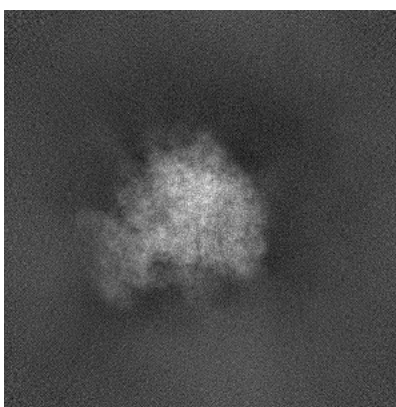


Z

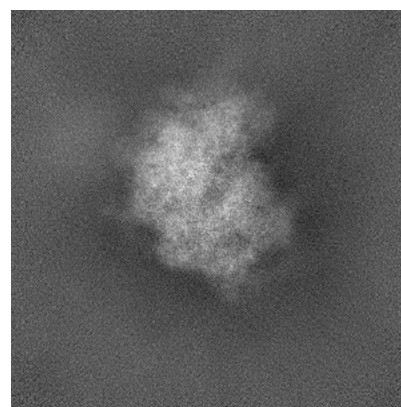
6.1.2 Raw map



X



Y

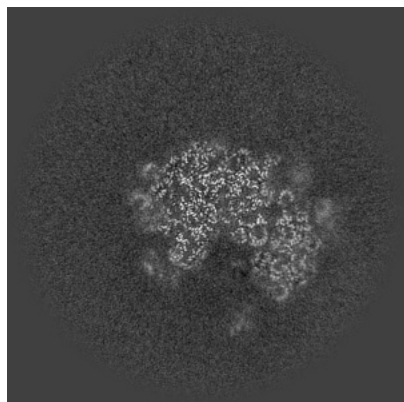


Z

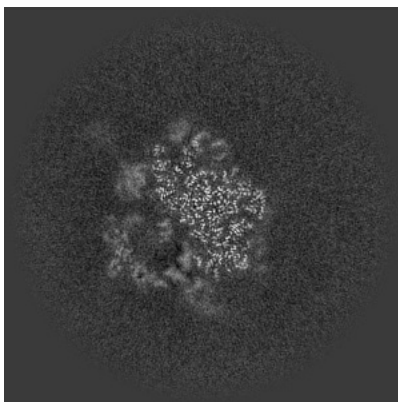
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

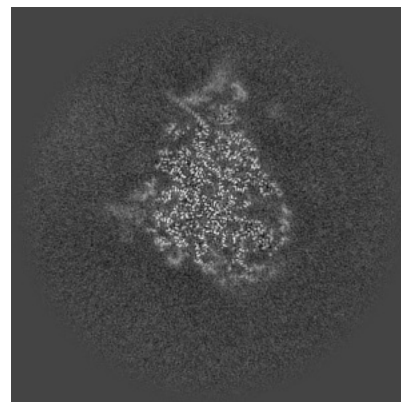
6.2.1 Primary map



X Index: 256

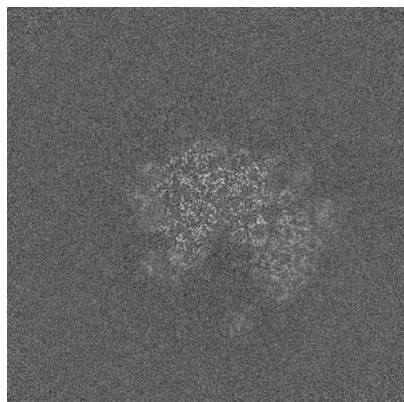


Y Index: 256

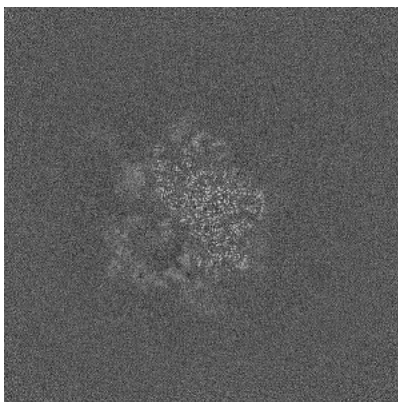


Z Index: 256

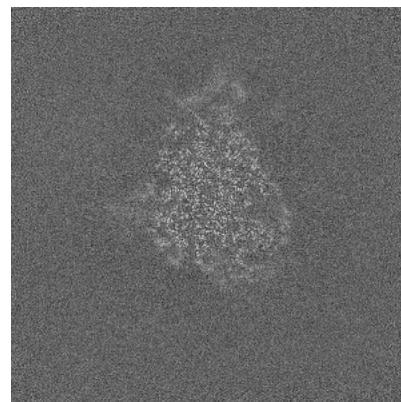
6.2.2 Raw map



X Index: 256



Y Index: 256

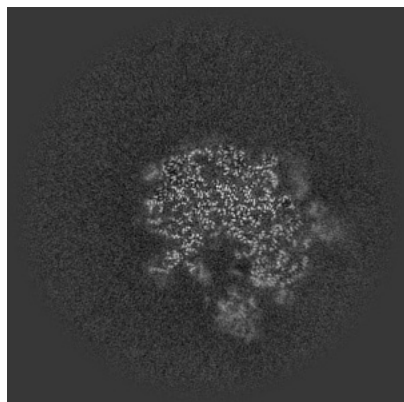


Z Index: 256

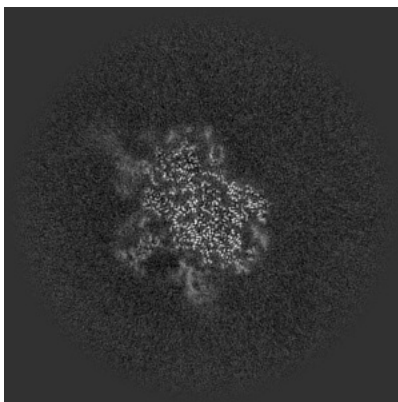
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

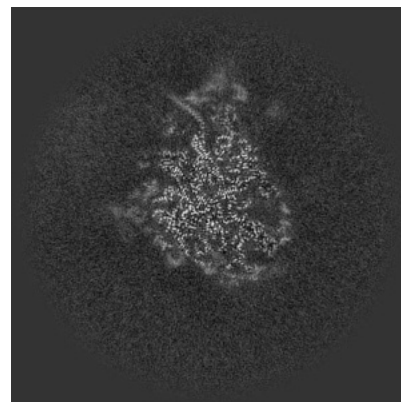
6.3.1 Primary map



X Index: 243

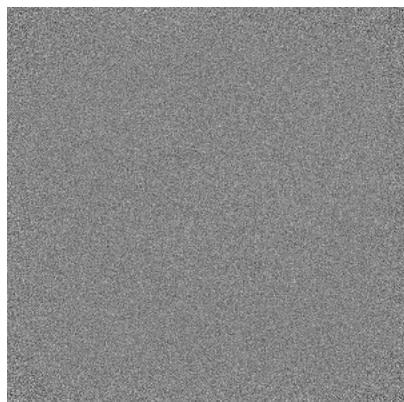


Y Index: 243

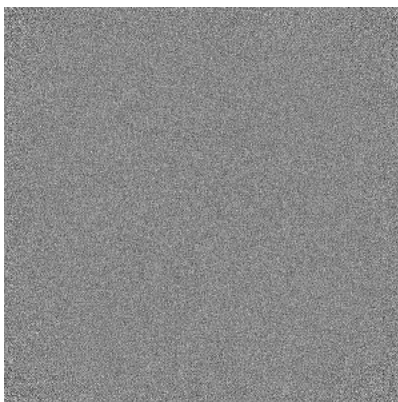


Z Index: 254

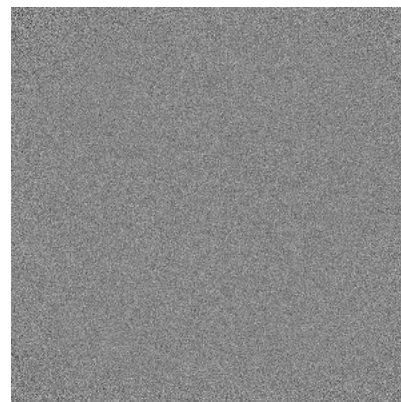
6.3.2 Raw map



X Index: 0



Y Index: 0

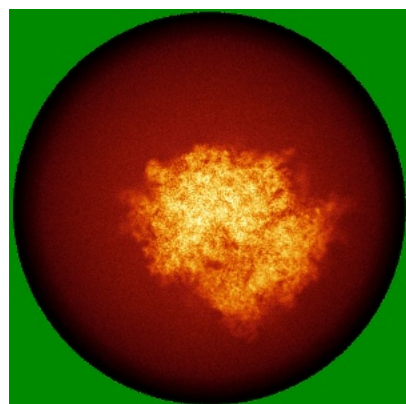


Z Index: 0

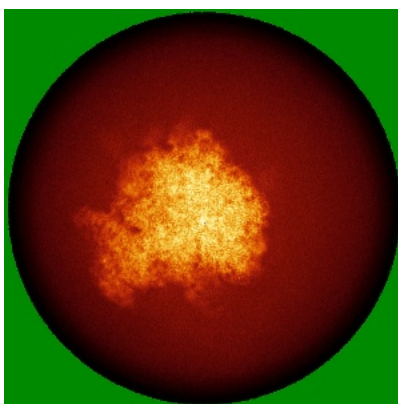
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

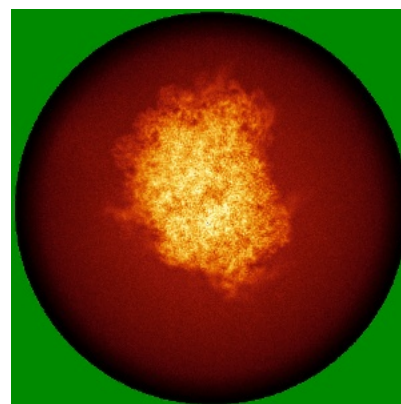
6.4.1 Primary map



X

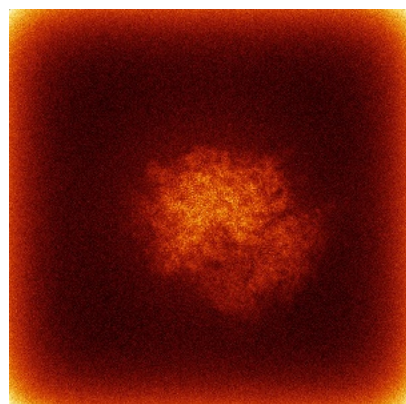


Y

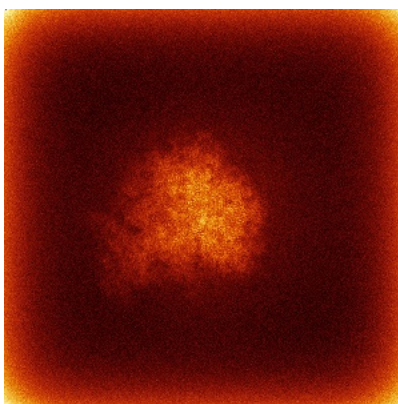


Z

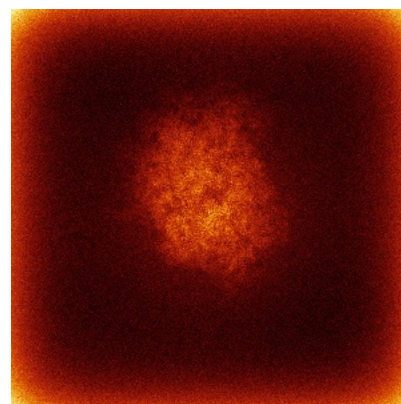
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



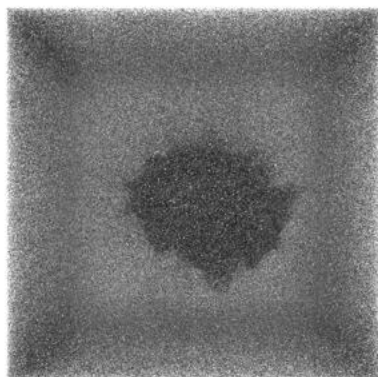
Y



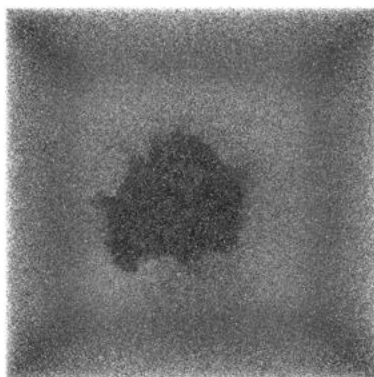
Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

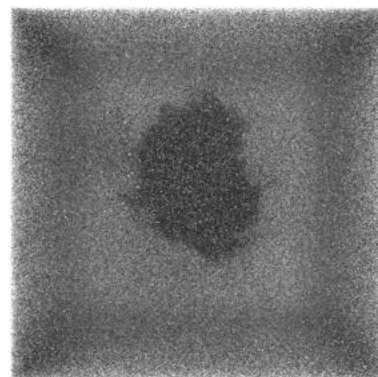
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

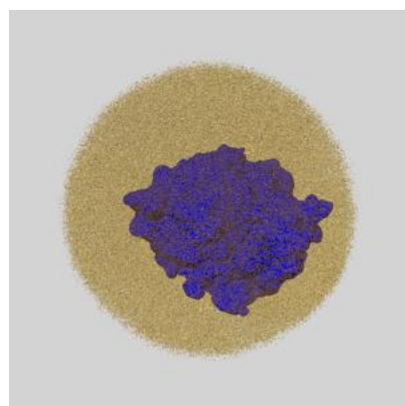
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

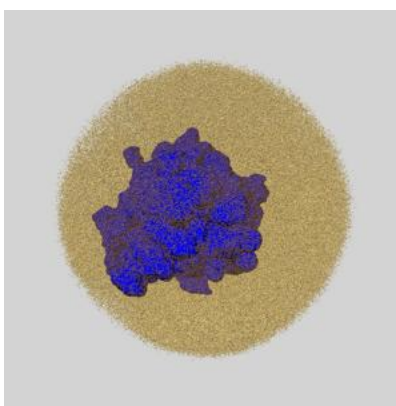
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

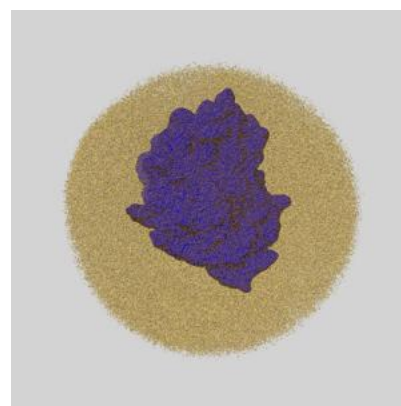
6.6.1 emd_71329_msk_1.map [i](#)



X



Y

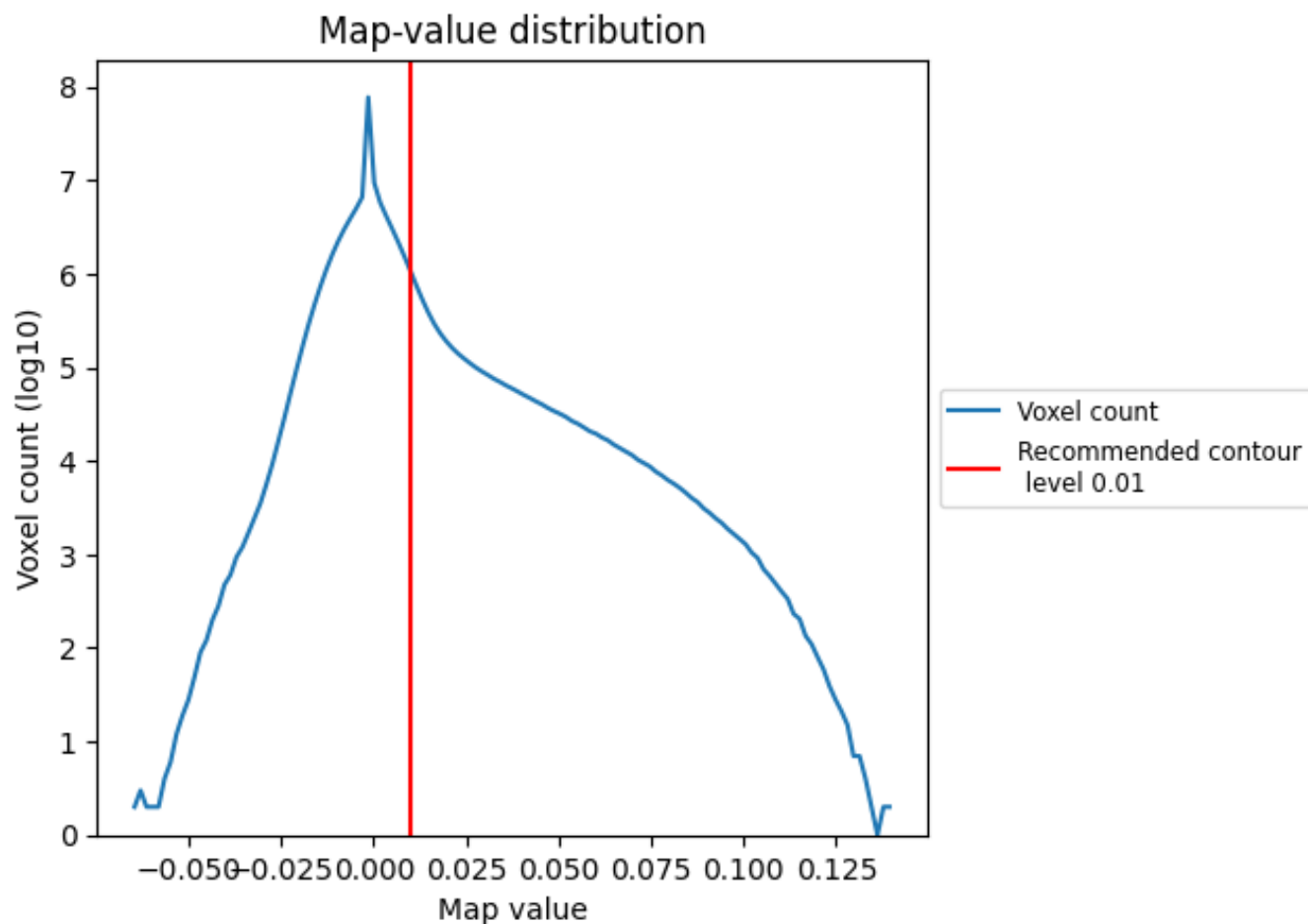


Z

7 Map analysis [i](#)

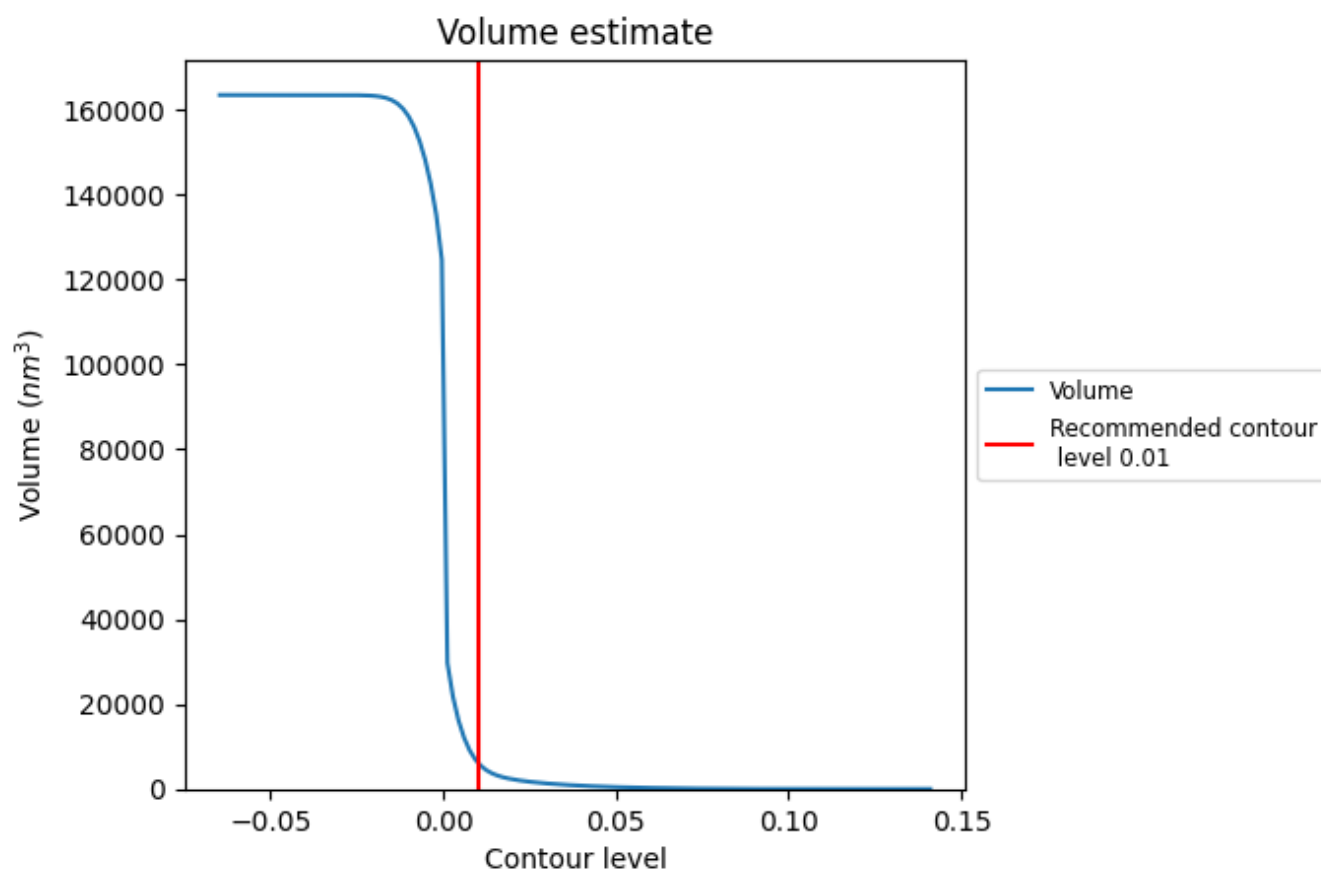
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

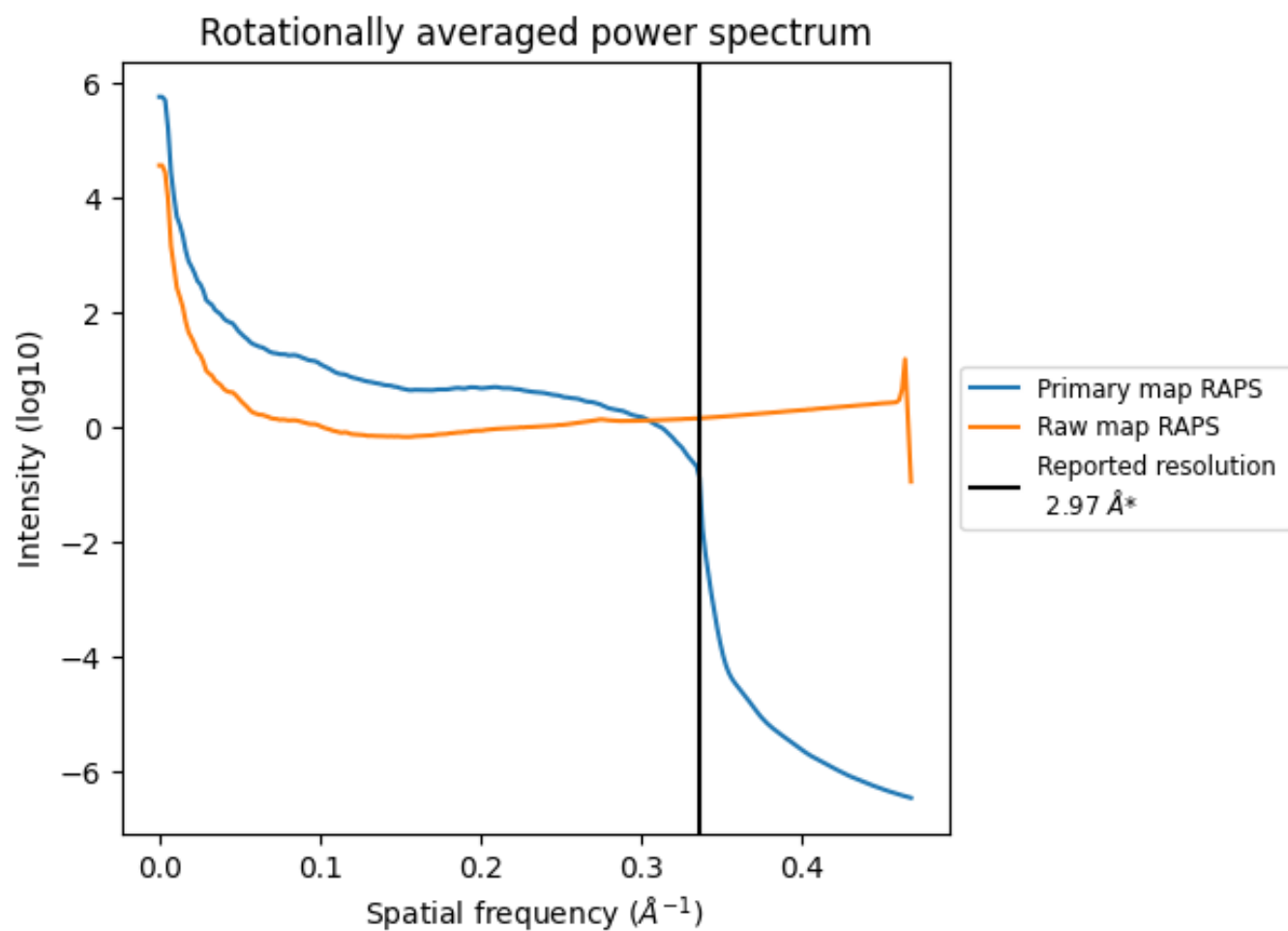
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6309 nm³; this corresponds to an approximate mass of 5699 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

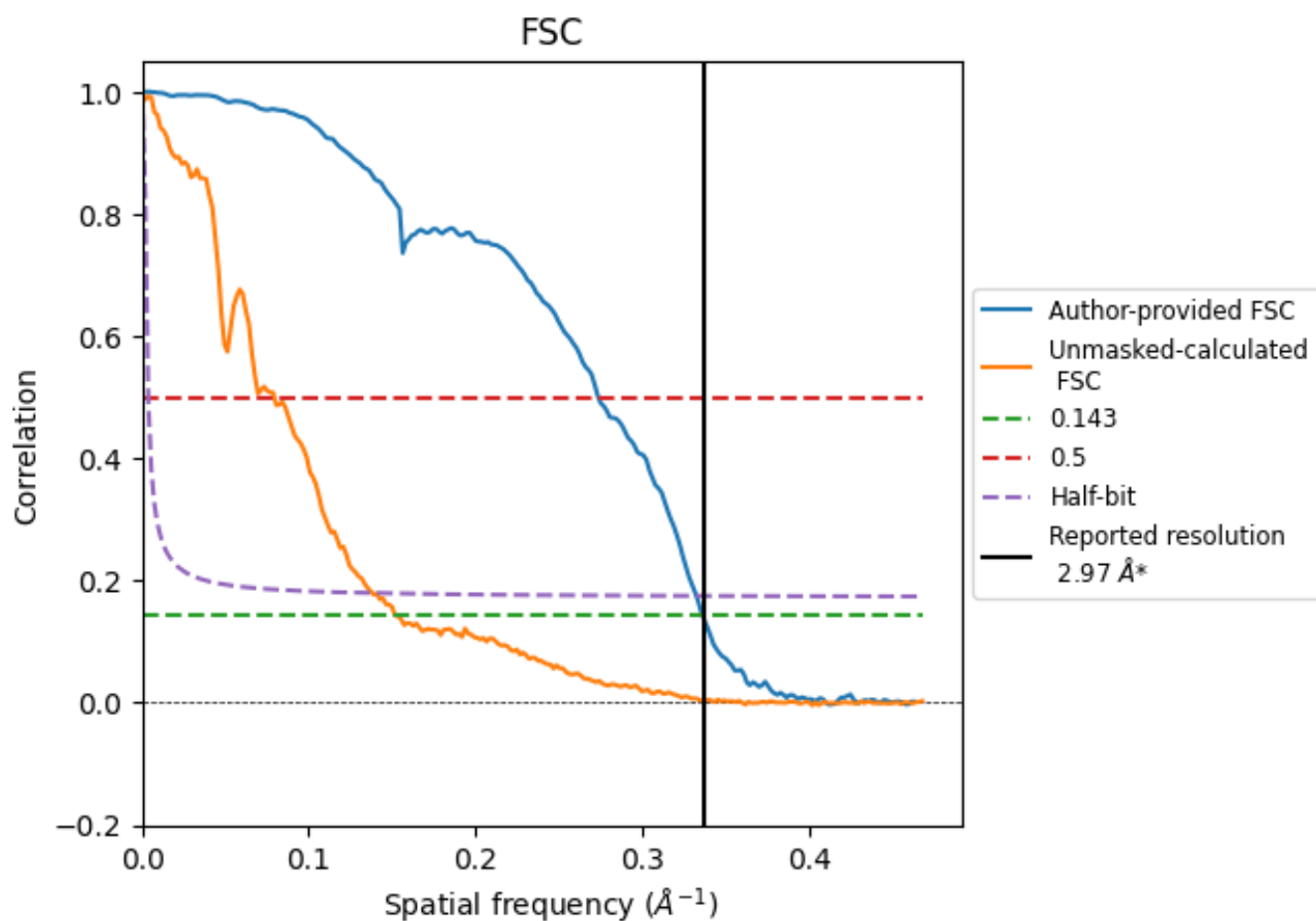


*Reported resolution corresponds to spatial frequency of 0.337 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.337 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

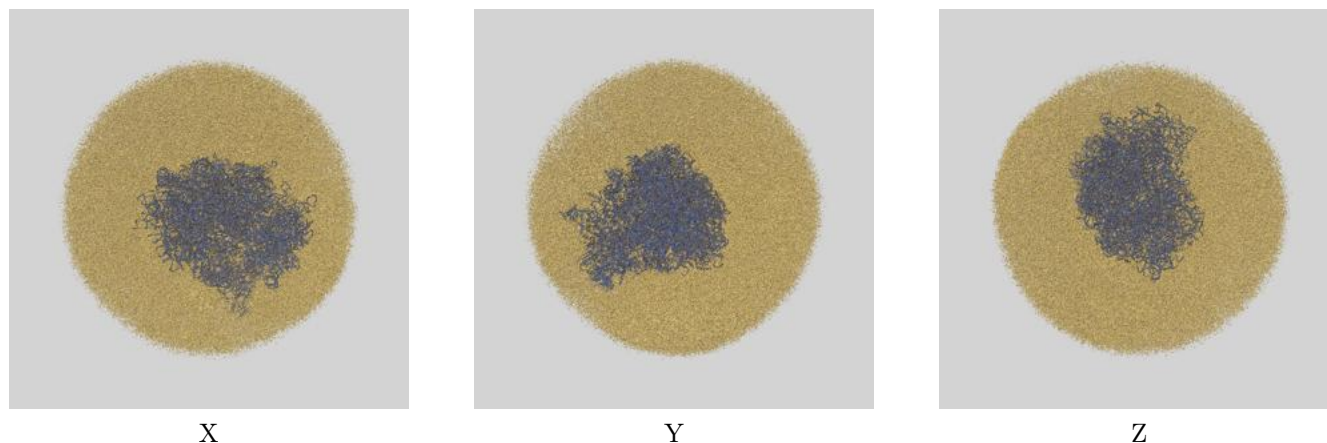
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.97	-	-
Author-provided FSC curve	2.97	3.65	3.01
Unmasked-calculated*	6.59	12.61	7.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.59 differs from the reported value 2.97 by more than 10 %

9 Map-model fit [i](#)

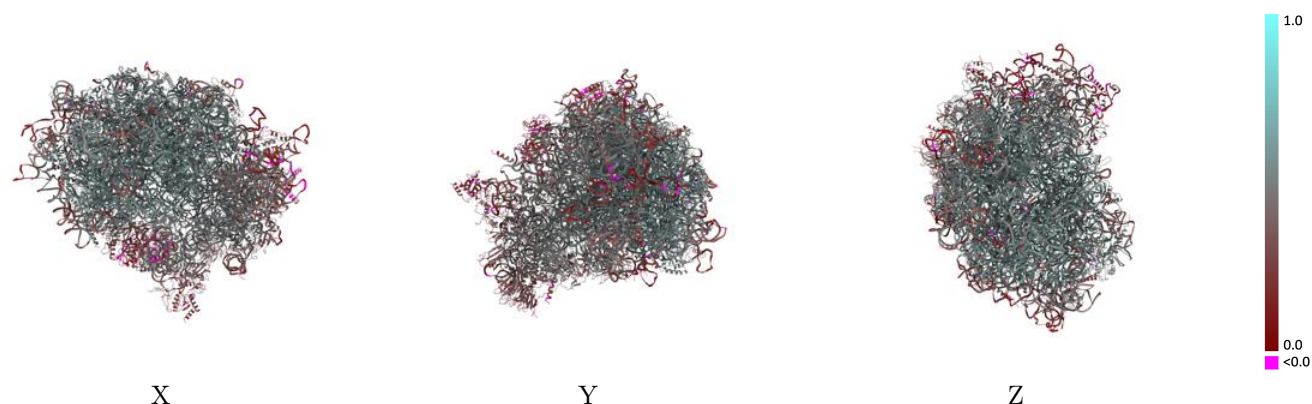
This section contains information regarding the fit between EMDB map EMD-71329 and PDB model 9P6Z. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



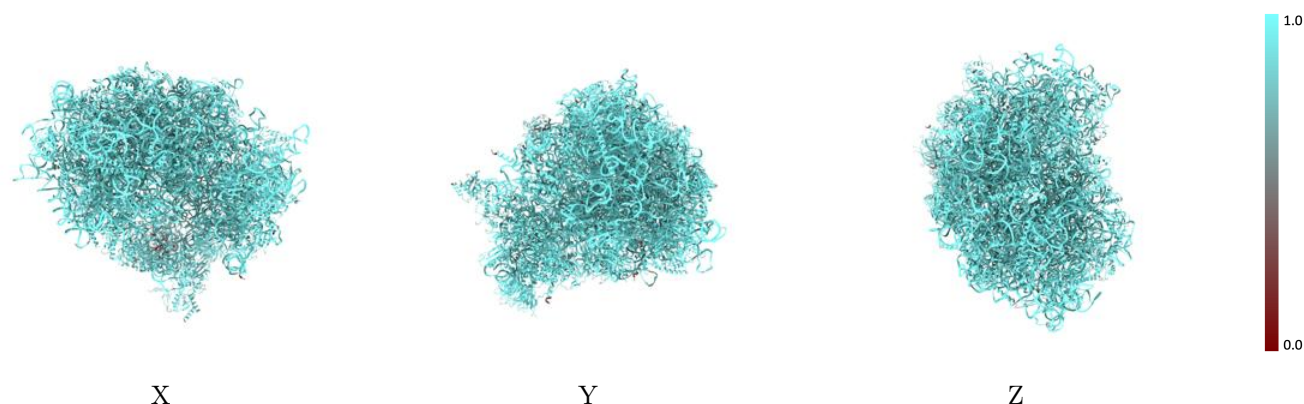
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



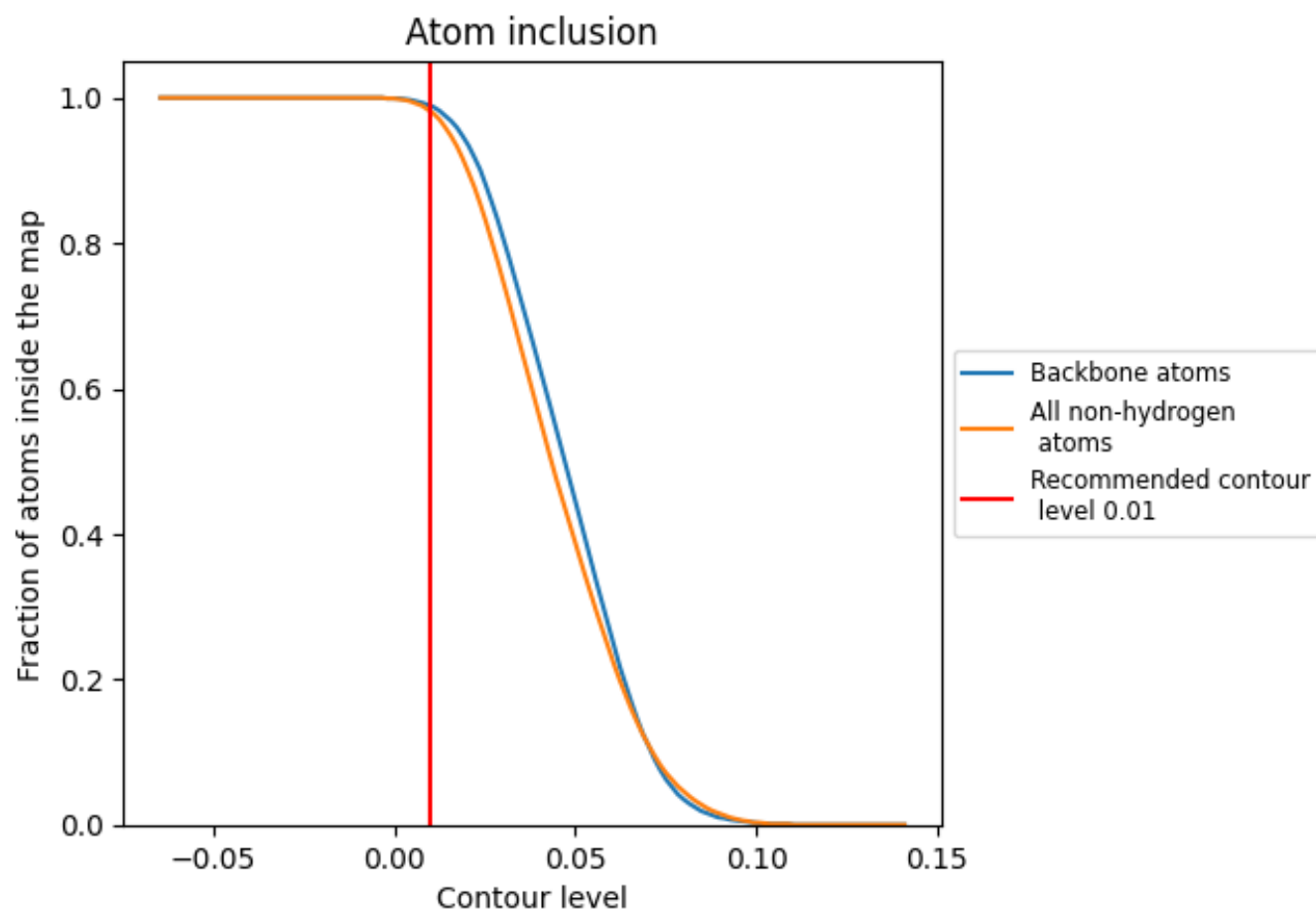
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9810	 0.4730
CI	 0.8620	 0.3560
L5	 0.9920	 0.4970
L7	 0.9990	 0.5400
L8	 0.9930	 0.5130
LA	 0.9940	 0.5620
LB	 0.9790	 0.5420
LC	 0.9810	 0.5370
LD	 0.9800	 0.4960
LE	 0.9730	 0.4750
LF	 0.9880	 0.5430
LG	 0.9550	 0.4790
LH	 0.9890	 0.5270
LI	 0.9810	 0.5300
LJ	 0.9640	 0.4790
LL	 0.9650	 0.5060
LM	 0.9870	 0.5190
LN	 0.9960	 0.5710
LO	 0.9890	 0.5410
LP	 0.9840	 0.5490
LQ	 0.9880	 0.5580
LR	 0.9550	 0.4860
LS	 0.9950	 0.5590
LT	 0.9800	 0.5230
LU	 0.9790	 0.4560
LV	 0.9880	 0.5520
LW	 0.9380	 0.3690
LX	 0.9790	 0.5270
LY	 0.9800	 0.5250
LZ	 0.9940	 0.5170
La	 0.9870	 0.5560
Lb	 0.9410	 0.4550
Lc	 0.9750	 0.5080
Ld	 0.9740	 0.5110
Le	 0.9900	 0.5560



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Chain	Atom inclusion	Q-score
Lf	 0.9940	 0.5680
Lg	 0.9840	 0.5280
Lh	 0.9820	 0.5090
Li	 0.9810	 0.5180
Lj	 0.9970	 0.5610
Lk	 0.9710	 0.4700
Ll	 0.9880	 0.5190
Lm	 0.9980	 0.5490
Ln	 0.9950	 0.5460
Lo	 0.9930	 0.5470
Lp	 0.9830	 0.5420
Lr	 0.9820	 0.5470
Ls	 0.7560	 0.1800
Lt	 0.7630	 0.1760
Pt	 0.9890	 0.4240
S2	 0.9940	 0.4440
SA	 0.9680	 0.4370
SB	 0.9640	 0.4680
SC	 0.9840	 0.4700
SD	 0.9700	 0.3850
SE	 0.9780	 0.4330
SF	 0.9620	 0.4150
SG	 0.9640	 0.3520
SH	 0.9460	 0.3640
SI	 0.9850	 0.4580
SJ	 0.9750	 0.4320
SK	 0.9520	 0.3480
SL	 0.9610	 0.4680
SM	 0.8620	 0.1770
SN	 0.9810	 0.4870
SO	 0.9620	 0.4770
SP	 0.9380	 0.3900
SQ	 0.9670	 0.4010
SR	 0.9550	 0.3980
SS	 0.9560	 0.4010
ST	 0.9740	 0.3850
SU	 0.9630	 0.3540
SV	 0.9780	 0.4550
SW	 0.9900	 0.4960
SX	 0.9780	 0.4970
SY	 0.9620	 0.3710
SZ	 0.9190	 0.3660

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Chain	Atom inclusion	Q-score
Sa	 0.9770	 0.4920
Sb	 0.9660	 0.4440
Sc	 0.9180	 0.3920
Sd	 0.9960	 0.4390
Se	 0.9170	 0.3680
Sf	 0.9010	 0.2460
Sg	 0.9610	 0.3140
Zt	 0.9400	 0.1770